GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:07:41 ; Search time 41.5664 Seconds
(without alignments)
2041.789 Million cell updates/sec

Title: US-09-830-328C-2
Perfect score: 1642
Sequence: 1 MAREDSVKCLRCLLYALNLL.....IFEHTSMANSFNTHFEMEEL 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1642	100.0	305	10	US-09-946-374-273	Sequence 273, App
2	1642	100.0	305	12	US-10-206-915-324	Sequence 324, App
3	1642	100.0	305	12	US-10-199-670-324	Sequence 324, App
4	1642	100.0	305	12	US-10-201-858-324	Sequence 324, App
5	1642	100.0	305	12	US-10-205-890-324	Sequence 324, App
6	1642	100.0	305	12	US-10-208-024-324	Sequence 324, App
7	1642	100.0	305	12	US-10-201-853-324	Sequence 324, App
8	1642	100.0	305	12	US-10-063-745-108	Sequence 108, App
9	1642	100.0	305	12	US-10-063-512-108	Sequence 108, App
10	1642	100.0	305	12	US-10-063-513-108	Sequence 108, App
11	1642	100.0	305	12	US-10-063-515-108	Sequence 108, App
12	1642	100.0	305	12	US-10-063-549-108	Sequence 108, App
13	1642	100.0	305	12	US-10-063-569-108	Sequence 108, App
14	1642	100.0	305	12	US-10-063-551-108	Sequence 108, App
15	1642	100.0	305	12	US-10-174-581-324	Sequence 324, App
16	1642	100.0	305	12	US-10-176-483-324	Sequence 324, App
17	1642	100.0	305	12	US-10-176-749-324	Sequence 324, App
18	1642	100.0	305	12	US-10-176-914-324	Sequence 324, App
19	1642	100.0	305	12	US-10-176-915-324	Sequence 324, App
20	1642	100.0	305	12	US-10-006-485A-273	Sequence 273, App
21	1642	100.0	305	12	US-10-013-907A-273	Sequence 273, App
22	1642	100.0	305	12	US-10-015-499A-273	Sequence 273, App
23	1642	100.0	305	12	US-10-063-555-108	Sequence 108, App
24	1642	100.0	305	12	US-10-063-563-108	Sequence 108, App
25	1642	100.0	305	12	US-10-063-594-108	Sequence 108, App
26	1642	100.0	305	12	US-10-063-553-108	Sequence 108, App
27	1642	100.0	305	12	US-10-063-554-108	Sequence 108, App
28	1642	100.0	305	12	US-10-176-484-324	Sequence 324, App
29	1642	100.0	305	12	US-10-180-550-324	Sequence 324, App
30	1642	100.0	305	12	US-10-183-014-324	Sequence 324, App
31	1642	100.0	305	12	US-10-187-738-324	Sequence 324, App
32	1642	100.0	305	12	US-10-187-740-324	Sequence 324, App
33	1642	100.0	305	12	US-10-187-883-324	Sequence 324, App
34	1642	100.0	305	12	US-10-194-363-324	Sequence 324, App
35	1642	100.0	305	12	US-10-194-460-324	Sequence 324, App
36	1642	100.0	305	12	US-10-194-463-324	Sequence 324, App
37	1642	100.0	305	12	US-10-194-484-324	Sequence 324, App
38	1642	100.0	305	12	US-10-195-884-324	Sequence 324, App
39	1642	100.0	305	12	US-10-195-896-324	Sequence 324, App
40	1642	100.0	305	12	US-10-196-744-324	Sequence 324, App
41	1642	100.0	305	12	US-10-196-755-324	Sequence 324, App
42	1642	100.0	305	12	US-10-196-757-324	Sequence 324, App
43	1642	100.0	305	12	US-10-197-704-324	Sequence 324, App
44	1642	100.0	305	12	US-10-197-710-324	Sequence 324, App
45	1642	100.0	305	12	US-10-198-758-324	Sequence 324, App

ALIGNMENTS

RESULT 1
US-09-946-374-273
; Sequence 273, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750

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← 3430A...
← 3230P1...
10/063616
10/063615
10/063724

154, 83,84

; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
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;  PRIOR APPLICATION NUMBER: 60/104987
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;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
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;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807

  Query Match             100.0%;  Score 1642;  DB 10;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
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Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
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Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
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Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305

RESULT 2
US-10-206-915-324
; Sequence 324, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C513
;  CURRENT APPLICATION NUMBER: US/10/206,915
;  CURRENT FILING DATE:  2002-07-26
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 324
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-206-915-324

  Query Match             100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
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Db        301 EMEEL 305

RESULT 3
US-10-199-670-324
; Sequence 324, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C401
;  CURRENT APPLICATION NUMBER: US/10/199,670
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;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 324
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-199-670-324

  Query Match           100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 4
US-10-201-858-324
; Sequence 324, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C464
;  CURRENT APPLICATION NUMBER: US/10/201,858
;  CURRENT FILING DATE:  2002-07-23
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 324
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-201-858-324

  Query Match           100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 5
US-10-205-890-324
; Sequence 324, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
```

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;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C519
;  CURRENT APPLICATION NUMBER: US/10/205,890
;  CURRENT FILING DATE:  2002-07-26
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 324
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-205-890-324

  Query Match             100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 6
US-10-208-024-324
; Sequence 324, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C538
;  CURRENT APPLICATION NUMBER: US/10/208,024
;  CURRENT FILING DATE:  2002-07-29
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 324
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-208-024-324

  Query Match             100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305
```

```
RESULT 7
US-10-201-853-324
; Sequence 324, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C465
;  CURRENT APPLICATION NUMBER: US/10/201,853
;  CURRENT FILING DATE:  2002-07-23
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 324
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-201-853-324

  Query Match             100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 8
US-10-063-745-108
; Sequence 108, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,745
;  CURRENT FILING DATE:  2002-05-09
;      Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-745-108

  Query Match             100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 9
US-10-063-512-108
; Sequence 108, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
```

```
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,512
;  CURRENT FILING DATE:  2002-05-01
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-512-108

  Query Match           100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 10
US-10-063-513-108
; Sequence 108, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,513
;  CURRENT FILING DATE:  2002-05-01
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-513-108

  Query Match           100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 11
US-10-063-515-108
; Sequence 108, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,515
;  CURRENT FILING DATE:  2002-05-01
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-515-108

  Query Match           100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity  100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
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Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 12
US-10-063-549-108
; Sequence 108, Application US/10063549
; Publication No. US20030027986A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,549
;  CURRENT FILING DATE:  2002-05-02
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-549-108

  Query Match             100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 13
US-10-063-569-108
; Sequence 108, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,569
;  CURRENT FILING DATE:  2002-05-02
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-569-108

  Query Match             100.0%;  Score 1642;  DB 12;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-163;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 14
US-10-063-551-108
; Sequence 108, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,551
;  CURRENT FILING DATE:  2002-05-02
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 108
;   LENGTH: 305
;   TYPE: PRT
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; ORGANISM: Homo Sapien
US-10-063-551-108

  Query Match 100.0%; Score 1642; DB 12; Length 305;
  Best Local Similarity 100.0%; Pred. No. 7.3e-163;
  Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305
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RESULT 15
US-10-174-581-324
; Sequence 324, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366

; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 1642; DB 12; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305
```

Search completed: May 13, 2004, 16:17:16
Job time : 43.5664 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:00:55 ; Search time 11.3363 Seconds
(without alignments)
1400.935 Million cell updates/sec

Title: US-09-830-328C-2
Perfect score: 1642
Sequence: 1 MAREDSVKCLRCLLYALNLL.....IFEHTSMANSFNTHFEMEEL 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1642	100.0	305	1	T412_HUMAN	O95859 homo sapien
2	292	17.8	253	1	C151_RAT	Q9qza6 rattus norv
3	284	17.3	253	1	C151_MOUSE	O35566 mus musculu
4	279	17.0	239	1	TNE5_HUMAN	O75954 homo sapien
5	272	16.6	253	1	C151_HUMAN	P48509 homo sapien
6	269	16.4	253	1	C151_CERAE	Q9mym2 cercopithec
7	264	16.1	238	1	T4S7_MOUSE	Q9dck3 mus musculu
8	259	15.8	238	1	T4S7_HUMAN	O14817 homo sapien
9	255.5	15.6	237	1	CD63_RABIT	Q28709 oryctolagus
10	250.5	15.3	237	1	CD63_HUMAN	P08962 homo sapien
11	244	14.9	236	1	CD63_BOVIN	Q9xsk2 bos taurus
12	237.5	14.5	237	1	CD63_RAT	P28648 rattus norv
13	237.5	14.5	267	1	CD82_HUMAN	P27701 homo sapien
14	227.5	13.9	237	1	CD63_MOUSE	P41731 mus musculu
15	220.5	13.4	225	1	CD9_PIG	Q8wmq3 sus scrofa
16	214.5	13.1	227	1	CD9_HUMAN	P21926 homo sapien
17	213.5	13.0	225	1	CD9_BOVIN	P30932 bos taurus
18	213.5	13.0	225	1	CD9_FELCA	P40239 felis silve
19	212.5	12.9	225	1	CD9_MOUSE	P40240 mus musculu
20	212.5	12.9	227	1	CD9_CERAE	P30409 cercopithec
21	211.5	12.9	225	1	CD9_RAT	P40241 rattus norv
22	210.5	12.8	221	1	TSN2_RAT	Q9jjw1 rattus norv
23	209.5	12.8	221	1	TSN2_MOUSE	Q922j6 mus musculu
24	204	12.4	237	1	T4S3_HUMAN	P19075 homo sapien
25	201	12.2	236	1	CD81_SAGOE	Q9n0j9 saguinus oe
26	199	12.1	236	1	CD81_HUMAN	P60033 homo sapien
27	199	12.1	236	1	CD81_PANTR	P60034 pan troglod
28	199	12.1	236	1	CD81_RAT	Q62745 rattus norv
29	193.5	11.8	218	1	CD53_MOUSE	Q61451 mus musculu
30	193	11.8	236	1	CD81_MOUSE	P35762 mus musculu
31	192.5	11.7	281	1	CD37_HUMAN	P11049 homo sapien
32	191	11.6	249	1	T4S2_HUMAN	P41732 homo sapien
33	190.5	11.6	221	1	TSN2_HUMAN	O60636 homo sapien
34	189	11.5	236	1	CD81_CERAE	O97703 cercopithec
35	189	11.5	249	1	T4S2_MOUSE	Q62283 mus musculu
36	189	11.5	253	1	T4S8_MOUSE	Q9qy33 mus musculu
37	187	11.4	245	1	T4S6_HUMAN	O43657 homo sapien
38	184.5	11.2	218	1	CD53_RAT	P24485 rattus norv
39	184	11.2	253	1	T4S8_HUMAN	O60637 homo sapien
40	178	10.8	245	1	T4S6_MOUSE	O70401 mus musculu
41	176	10.7	204	1	T413_HUMAN	O95857 homo sapien
42	175.5	10.7	281	1	CD37_MOUSE	Q61470 mus musculu
43	175	10.7	266	1	CD82_MOUSE	P40237 mus musculu
44	175	10.7	268	1	T4S9_HUMAN	O60628 homo sapien
45	174.5	10.6	219	1	CD53_HUMAN	P19397 homo sapien

ALIGNMENTS

RESULT 1
T412_HUMAN
ID T412_HUMAN STANDARD; PRT; 305 AA.
AC O95859;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transmembrane 4 superfamily member 12 (Tetraspan NET-2).
GN TM4SF12 OR NET2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20185353; PubMed=10719184;
RA Serru V., Dessen P., Boucheix C., Rubinstein E.;
RT "Sequence and expression of seven new tetraspans.";
RL Biochim. Biophys. Acta 1478:159-163(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC ---

CC ---
DR EMBL; AF124522; AAD17317.1; -.
DR Genew; HGNC:21641; TM4SF12.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; FALSE_NEG.
KW Transmembrane.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 33 POTENTIAL.
FT DOMAIN 34 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 80 POTENTIAL.
FT DOMAIN 81 89 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 90 110 POTENTIAL.
FT DOMAIN 111 224 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 225 245 POTENTIAL.
FT DOMAIN 246 305 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 305 AA; 35382 MW; EBF4D5E1371E92DC CRC64;

Query Match 100.0%; Score 1642; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 9e-134;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

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Db          1 MAREDSVKCLRCLLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305
```

RESULT 2
C151_RAT
ID C151_RAT STANDARD; PRT; 253 AA.
AC Q9QZA6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Platelet endothelial tetraspan antigen 3 (CD151 antigen).
GN CD151 OR PETA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=21539251; PubMed=11682256;
RA Hua L.V., Green M., Wong A., Warsh J.J., Li P.P.;
RT "Tetraspan protein CD151: a common target of mood stabilizing drugs?";
RL Neuropsychopharmacology 25:729-736(2001).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC ---
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CC ---
DR EMBL; AF192547; AAF05763.2; -.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Transmembrane; Lipoprotein; Palmitate.

FT	DOMAIN	1	18 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	19	39 POTENTIAL.
FT	DOMAIN	40	57 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	58	78 POTENTIAL.
FT	DOMAIN	79	91 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	92	112 POTENTIAL.
FT	DOMAIN	113	221 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	222	242 POTENTIAL.
FT	DOMAIN	243	253 CYTOPLASMIC (POTENTIAL).
FT	LIPID	11	11 S-palmitoyl cysteine (By similarity).
FT	LIPID	15	15 S-palmitoyl cysteine (By similarity).
FT	LIPID	242	242 S-palmitoyl cysteine (By similarity).
FT	LIPID	243	243 S-palmitoyl cysteine (By similarity).
FT	CARBOHYD	159	159 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 253 AA; 28355 MW; 51876AF31B4DCB2B CRC64;

```
  Query Match            17.8%;  Score 292;  DB 1;  Length 253;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-18;
  Matches   76;  Conservative   48;  Mismatches   96;  Indels   34;  Gaps    9;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| | :         ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASS--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWS 126
                 ::: |:|| | | |    ||  ||  ||:|| :|:  |:  : | |:|   :: :
Db         66 VAGVVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYVYYQQLNTELKEN 125

Qy        127 DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW---------- 176
              |:  |   |  :  :|:| :  |:|| |||     ||    : :|
Db        126 LKDTMIKRYHQSG---HEGVTNAVDKLQQEFHCCGSNNSRDW---RDSEWIRSGEADSRV 179

Qy        177 PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQ 234
              |||||     || |: |    |::|  : ||  |: ||::  : |:|:  :|| |   |
Db        180 VPDSCCKTVVTGCGKREH---ASNIYKVEGGCITKLESFIQ--EHLRVIGAVGIGIACVQ 234

Qy        235 ILAMILTITLLWAL 248
              :  || |  |  :|
Db        235 VFGMIFTCCLYRSL 248
```

RESULT 3
C151_MOUSE
ID C151_MOUSE STANDARD; PRT; 253 AA.
AC O35566; O89118;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Platelet-endothelial tetraspan antigen 3 (PETA-3) (GP27) (Membrane
DE glycoprotein SFA-1) (CD151 antigen).
GN CD151 OR PETA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97438231; PubMed=9294006;
RA Hasegawa H., Watanabe H., Nomura T., Utsunomiya Y., Yanagisawa K.,
RA Fujita S.;
RT "Molecular cloning and expression of mouse homologue of SFA-1/PETA-3
RT (CD151), a member of the transmembrane 4 superfamily.";
RL Biochim. Biophys. Acta 1353:125-130(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=98267146; PubMed=9602068;
RA Fitter S., Seldin M.F., Ashman L.K.;
RT "Characterisation of the mouse homologue of CD151 (PETA-3/SFA-1);
RT genomic structure, chromosomal localisation and identification of 2
RT novel splice forms.";
RL Biochim. Biophys. Acta 1398:75-85(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC ---
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CC ---
DR EMBL; D89290; BAA22447.1; -.
DR EMBL; AF033620; AAC25952.1; -.
DR EMBL; U89772; AAC25976.1; -.

```
DR   MGD; MGI:1096360; Cd151.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Transmembrane; Lipoprotein; Palmitate.
FT   DOMAIN        1     18       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     19     39       POTENTIAL.
FT   DOMAIN       40     57       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     58     78       POTENTIAL.
FT   DOMAIN       79     91       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     92    112       POTENTIAL.
FT   DOMAIN      113    221       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    222    242       POTENTIAL.
FT   DOMAIN      243    253       CYTOPLASMIC (POTENTIAL).
FT   LIPID        11     11       S-palmitoyl cysteine (By similarity).
FT   LIPID        15     15       S-palmitoyl cysteine (By similarity).
FT   LIPID       242    242       S-palmitoyl cysteine (By similarity).
FT   LIPID       243    243       S-palmitoyl cysteine (By similarity).
FT   CARBOHYD    159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    237    237       G -> S (IN REF. 1).
SQ   SEQUENCE   253 AA;  28246 MW;  AEBEEBCE2D765F1B CRC64;

  Query Match             17.3%;  Score 284;  DB 1;  Length 253;
  Best Local Similarity   29.3%;  Pred. No. 2.6e-17;
  Matches   76;  Conservative   45;  Mismatches   94;  Indels   44;  Gaps   10;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| | :        ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASS--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWS 126
                 ::: |:|| | | |    || ||  ||:|| :|:  |:  : | |:|
Db         66 VAGVVVMVTGVLGCCATPKERRNLLRLYFILLLIIFLLEIIAGILAYVYYQQL------- 118

Qy        127 DMVTLKARMTNYGLPRYRWLTH-----AWNFFQREFKCCGVVYFTDWLEMTEMDW----- 176
               ||  : :  : ||    |     | :  |:|| |||     ||    : :|
Db        119 -NTELKENLKDTMVKRYHQSGHEGVSSAVDKLQQEFHCCGSNNSQDW---QDSEWIRSGE 174

Qy        177 -----PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGIS 229
                  |||||     || |: |    |::|  : ||  |: :|::  : |:|:  :||
Db        175 ADSRVVPDSCCKTMVAGCGKRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIG 229

Qy        230 IGVTQILAMILTITLLWAL 248
              |   |:  || |  |  :|
Db        230 IACVQVFGMIFTCCLYRSL 248


RESULT 4
TNE5_HUMAN
ID   TNE5_HUMAN     STANDARD;      PRT;   239 AA.
AC   O75954;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tetraspan NET-5.
GN   NET5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20185353; PubMed=10719184;
RA   Serru V., Dessen P., Boucheix C., Rubinstein E.;
RT   "Sequence and expression of seven new tetraspans.";
RL   Biochim. Biophys. Acta 1478:159-163(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF089749; AAC35859.1; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Transmembrane.
FT   DOMAIN        1     13       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     14     34       POTENTIAL.
FT   DOMAIN       35     55       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     56     76       POTENTIAL.
FT   DOMAIN       77     85       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     86    106       POTENTIAL.
FT   DOMAIN      107    203       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    204    224       POTENTIAL.
FT   DOMAIN      225    239       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   239 AA;  26779 MW;  DD7BA332BF6584EB CRC64;

  Query Match             17.0%;  Score 279;  DB 1;  Length 239;
  Best Local Similarity   28.9%;  Pred. No. 6.6e-17;
  Matches   74;  Conservative   41;  Mismatches  103;  Indels   38;  Gaps    7;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHP--V 66
              ||: :::  ||:|||    :| |  |:     |  | :                || :   :
Db          8 CLKYMMFLFNLIFWLCGCGLLGVGIWLSVSQGNFATFSPS----------FPSLSAANL 56

Qy         67 MIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS 126
              :||:   ::: | ||  | :| |  ||  :|  ||||   ||          |::   :
Db         57 VIAIGTIVMVTGFLGCLGAIKENKCLLLSFFIVLLVILLAELIL--------LILFFVYM 108

Qy        127 DMVT------LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              | |        ||  :  |       | :|||  | | :|||  :|||  :   :  ||
Db        109 DKVNENAKKDLKEGLLLYHTENNVGLKNAWNIIQAEMRCCGVTDYTDWYPVLGENTVPDR 168

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||:    || : |     : |:: || :|:  :    |  ||  :|: | : ||| |
Db        169 CCMENSQGCGRNA----TTPLWRTGCYEKVKMWFDDNK--HVLGTVGMCILIMQILGMAF 222

Qy        241 TITLLWALY-----YD 251
              ::||   ::     ||
Db        223 SMTLFQHIHRTGKKYD 238


RESULT 5
C151_HUMAN
ID   C151_HUMAN     STANDARD;      PRT;   253 AA.
AC   P48509; Q14826; Q96TE3;
DT   01-FEB-1996 (Rel. 33, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Platelet-endothelial tetraspan antigen 3 (PETA-3) (GP27) (Membrane
DE   glycoprotein SFA-1) (CD151 antigen).
GN   CD151.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Platelet;
RX   MEDLINE=95359431; PubMed=7632941;
RA   Fitter S., Tetaz T.J., Berndt M.C., Ashman L.K.;
RT   "Molecular cloning of cDNA encoding a novel platelet-endothelial cell
RT   tetra-span antigen, PETA-3.";
RL   Blood 86:1348-1355(1995).
RN   [2]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=96186759; PubMed=8627808;
RA   Hasegawa H., Utsunomiya Y., Kishimoto K., Yanagisawa K., Fujita S.;
RT   "SFA-1, a novel cellular gene induced by human T-cell leukemia virus
RT   type 1, is a member of the transmembrane 4 superfamily.";
RL   J. Virol. 70:3258-3263(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   PubMed=11181065;
RA   Whittock N.V., McLean W.H.I.;
RT   "Genomic organization, amplification, fine mapping, and intragenic
RT   polymorphisms of the human hemidesmosomal tetraspanin CD151 gene.";
RL   Biochem. Biophys. Res. Commun. 281:425-430(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon, and Kidney;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   PALMITOYLATION.
RX   MEDLINE=21904786; PubMed=11907260;
RA   Yang X., Claas C., Kraeft S.K., Chen L.B., Wang Z., Kreidberg J.A.,
RA   Hemler M.E.;
RT   "Palmitoylation of tetraspanin proteins: modulation of CD151 lateral
RT   interactions, subcellular distribution, and integrin-dependent cell
RT   morphology.";
RL   Mol. Biol. Cell 13:767-781(2002).
CC   -!- SUBUNIT: Interacts with integrins alpha3beta1, alpha5beta1,
CC       alpha3beta1 and alpha6beta4, with CD9 and CD181.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in a variety of tissues including
CC       vascular endothelium and epidermis.
CC   -!- INDUCTION: BY HTLV-1.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD151 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd151.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U14650; AAA87064.1; -.
DR   EMBL; D29963; BAA06229.1; -.
DR   EMBL; AF315942; AAK14179.1; -.
DR   EMBL; BC001374; AAH01374.1; -.
DR   EMBL; BC013302; AAH13302.1; -.
DR   Genew; HGNC:1630; CD151.
DR   MIM; 602243; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Transmembrane; Polymorphism; Lipoprotein; Palmitate.
FT   DOMAIN        1     18       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     19     39       POTENTIAL.
FT   DOMAIN       40     57       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     58     78       POTENTIAL.
FT   DOMAIN       79     91       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     92    112       POTENTIAL.
FT   DOMAIN      113    221       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    222    242       POTENTIAL.
FT   DOMAIN      243    253       CYTOPLASMIC (POTENTIAL).
FT   LIPID        11     11       S-palmitoyl cysteine.
FT   LIPID        15     15       S-palmitoyl cysteine.
FT   LIPID       242    242       S-palmitoyl cysteine.
FT   LIPID       243    243       S-palmitoyl cysteine.
FT   CARBOHYD    159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     132    132       R -> K.
FT                                /FTId=VAR_012490.
FT   VARIANT     137    137       S -> P.
FT                                /FTId=VAR_012491.
SQ   SEQUENCE   253 AA;  28313 MW;  5C81D7D62D750EAF CRC64;

  Query Match             16.6%;  Score 272;  DB 1;  Length 253;
  Best Local Similarity   29.4%;  Pred. No. 2.8e-16;
  Matches   75;  Conservative   46;  Mismatches   98;  Indels   36;  Gaps   10;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| |          ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASG--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWS 126
                 ::: |:|| | | |    ||  ||  ||:|| :|:  |:  : | |:|   ::
Db         66 VAGTVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYAYYQQLNTELK-- 123

Qy        127 DMVTLKARMT-NYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW--------- 176
               ||  ||  |    :  :| | :  |:|| |||     ||    : :|
Db        124 --ENLKDTMTRRYHQSGHEAVTSAVDQLQQEFHCCGSNNSQDW---RDSEWIRSQEAGGR 178

Qy        177 -PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIGVT 233
              |||||      | :: |   |::|  : ||  |: :|::  :  |:|:  :|| |
Db        179 VVPDSCCKTVVALCGQRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIACV 233

Qy        234 QILAMILTITLLWAL 248
              |:  || |  |  :|
Db        234 QVFGMIFTCCLYRSL 248


RESULT 6
C151_CERAE
ID   C151_CERAE     STANDARD;      PRT;   253 AA.
AC   Q9MYM2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Platelet-endothelial tetraspan antigen 3 (PETA-3) (CD151 antigen).
GN   CD151.
OS   Cercopithecus aethiops (Green monkey) (Grivet), and
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534, 9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shanmukhappa K., Kapil S.;
RT   "CD151/PETA-3, a tetraspanin molecule, interacts with the 3'
RT   untranslated region and partial nucleoprotein gene of porcine
RT   reproductive and respiratory syndrome virus RNA.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
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CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF275665; AAF90151.1; -.
DR   EMBL; AF275666; AAF90152.1; -.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Transmembrane; Lipoprotein; Palmitate.
FT   DOMAIN        1     18       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     19     39       POTENTIAL.
FT   DOMAIN       40     57       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     58     78       POTENTIAL.
FT   DOMAIN       79     91       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     92    112       POTENTIAL.
FT   DOMAIN      113    221       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    222    242       POTENTIAL.
FT   DOMAIN      243    253       CYTOPLASMIC (POTENTIAL).
FT   LIPID        11     11       S-palmitoyl cysteine (By similarity).
FT   LIPID        15     15       S-palmitoyl cysteine (By similarity).
FT   LIPID       242    242       S-palmitoyl cysteine (By similarity).
FT   LIPID       243    243       S-palmitoyl cysteine (By similarity).
FT   CARBOHYD    159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   253 AA;  28438 MW;  CAD2780B63F644A4 CRC64;

  Query Match             16.4%;  Score 269;  DB 1;  Length 253;
  Best Local Similarity   28.6%;  Pred. No. 5.1e-16;
  Matches   72;  Conservative   48;  Mismatches  102;  Indels   30;  Gaps    8;

Qy           9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
               ||: ||:  |  |||  ::|:||  |     :: ::| |          ||    : :::
Db          15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASG--------TYLATAY-ILV 65

Qy          69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWS 126
                  ::: |:|| | | |    ||  || ||:|| :|:  ||  : | |:|   :: :
Db          66 VAGAVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGVLAYVYYQQLNTELKEN 125

Qy         127 DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW---------- 176
                 |:  |   | | :  :| | :  |:|| |||     ||    : :|
Db         126 LKDTMAKR---YHQPGHEAVTSAVDQLQQEFHCCGSNNSQDW---RDSEWIRLREARGRV 179

Qy         177 PPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQIL 236
                |||||     || :: |  ::  : : |   |: :|::  : |:|:  :|  |   |:
Db         180 VPDSCCKTVVAGCGQRDHAFNIYKV-EGGFITKLETFIQ--EHLRVIGAVGTGIACVQVF 236

Qy         237 AMILTITLLWAL 248
                || |  | :|
Db         237 GMIFTCCLYRSL 248


RESULT 7
T4S7_MOUSE
ID   T4S7_MOUSE     STANDARD;      PRT;   238 AA.
AC   Q9DCK3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Transmembrane 4 superfamily, member 7.
GN   TM4SF7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBUNIT: FORMS A COMPLEX WITH INTEGRINS (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AK002709; BAB22301.1; -.
DR   EMBL; BC003482; AAH03482.1; -.
DR   MGD; MGI:1928097; Tm4sf7.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Transmembrane.
FT   DOMAIN        1     13       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     14     34       POTENTIAL.
FT   DOMAIN       35     55       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     56     76       POTENTIAL.
FT   DOMAIN       77     85       CYTOPLASMIC (POTENTIAL). .
FT   TRANSMEM     86    106       POTENTIAL.
FT   DOMAIN      107    201       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    202    222       POTENTIAL.
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FT   DOMAIN      223    238       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   238 AA;  26053 MW;  AA916EF6078777FA CRC64;

  Query Match             16.1%;  Score 264;  DB 1;  Length 238;
  Best Local Similarity   28.3%;  Pred. No. 1.3e-15;
  Matches   73;  Conservative   46;  Mismatches   93;  Indels   46;  Gaps    9;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |||   :: :: |::| ||||||    || |  |:     |  ||::           |
Db          1 MAR-GCLQGVKYLMFAFNLLFWLGGCGVLGVGIWLAATQGNFATLSSS----------F 48

Qy         61 PVVHP--VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQE 118
              | :    ::|    |:: :| :|  | :| |  ||  :|  ||::| :|    |  :
Db         49 PSLSAANLLIVTGTFVMAIGFVGCIGALKENKCLLLTFFVLLLLVFLLEATIAVLFF--- 105

Qy        119 LMVPVQWSDMV------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMT 172
                :|| :         ||  :  ||      ||:||:  | :|:|||| :||| |:
Db        106 -----AYSDKIDSYAQQDLKKGLHLYGTQGNVGLTNAWSIIQTDFRCCGVSNYTDWFEVY 160

Qy        173 EMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEG------CGKKMYSFLRGTKQLQVLRFL 226
                |||||: ||          |   |:: |       | : : ::|:  : |  :
Db        161 NATRVPDSCCL-EF---------SDSCGLHEPGTWWKSPCYETVKAWLQ--ENLLAVGIF 208

Qy        227 GISIGVTQILAMILTITL 244
              |:   : ||| :   :|:
Db        209 GLCTALVQILGLTFAMTM 226


RESULT 8
T4S7_HUMAN
ID   T4S7_HUMAN     STANDARD;      PRT;   238 AA.
AC   O14817;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Transmembrane 4 superfamily, member 7 (Novel antigen 2) (NAG-2)
DE   (Tetraspanin 4) (Tspan-4).
GN   TM4SF7 OR NAG2 OR TSPAN4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98030601; PubMed=9360996;
RA   Tachibana I., Bodorova J., Berditchevski F., Zutter M.M., Hemler M.E.;
RT   "NAG-2, a novel transmembrane-4 superfamily (TM4SF) protein that
RT   complexes with integrins and other TM4SF proteins.";
RL   J. Biol. Chem. 272:29181-29189(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98390278; PubMed=9714763;
RA   Todd S.C., Doctor V.S., Levy S.;
RT   "Sequences and expression of six new members of the tetraspanin/TM4SF
RT   family.";
RL   Biochim. Biophys. Acta 1399:101-104(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBUNIT: FORMS A COMPLEX WITH INTEGRINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MULTIPLE TISSUES BUT IS ABSENT IN
CC       BRAIN, LYMPHOID CELLS, AND PLATELETS.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF022813; AAC51864.1; -.
DR   EMBL; AF054841; AAC69717.1; -.
DR   EMBL; BC000389; AAH00389.1; -.
DR   EMBL; BC019314; AAH19314.1; -.
DR   PIR; A59265; A59265.
DR   Genew; HGNC:11859; TM4SF7.
DR   MIM; 602644; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0006461; P:protein complex assembly; TAS.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Transmembrane.
FT   DOMAIN        1     13       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     14     34       POTENTIAL.
FT   DOMAIN       35     55       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     56     76       POTENTIAL.
FT   DOMAIN       77     85       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     86    106       POTENTIAL.
FT   DOMAIN      107    201       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    202    222       POTENTIAL.
FT   DOMAIN      223    238       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   238 AA;  26118 MW;  A6B9A5633065A492 CRC64;

  Query Match             15.8%;  Score 259;  DB 1;  Length 238;
  Best Local Similarity   27.0%;  Pred. No. 3.4e-15;
  Matches   68;  Conservative   48;  Mismatches  102;  Indels   34;  Gaps    7;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |||   :: :: |::| ||||||    || |  |:          | |:   | : : |
Db          1 MARA-CLQAVKYLMFAFNLLFWLGGCGVLGVGIWL----------AATQGSFATLSSSF 48

Qy         61 PVVHP--VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQE 118
              | :    ::|    |:: :| :|  | :| |  ||  :|  ||::| :|    |  :
Db         49 PSLSAANLLIITGAFVMAIGFVGCLGAIKENKCLLLTFFLLLLVFLLEATIAILFF--- 105

Qy        119 LMVPVQWSDMV------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMT 172
                ::| :         ||  :  ||      ||:||:  | :|:|||| :||| |:
Db        106 -----AYTDKIDRYAQQDLKKGLHLYGTQGNVGLTNAWSIIQTDFRCCGVSNYTDWFEVY 160

Qy        173 EMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGV 232
                |||||:      |   |       ::  | .: :  :|:  : |  :   |:   :
Db        161 NATRVPDSCCLEFSESCGLHAP----GTWWKAPCYETVKVWLQ--ENLLAVGIFGLCTAL 214

Qy        233 TQILAMILTITL 244
              |||  :   :|:
Db        215 VQILGLTFAMTM 226
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RESULT 9
CD63_RABIT
ID   CD63_RABIT     STANDARD;      PRT;   237 AA.
AC   Q28709;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   CD63 antigen.
GN   CD63.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=95120837; PubMed=7820873;
RA   Sohma Y., Suzuki T., Sasano H., Nagura H., Nose M., Yamamoto T.;
RT   "Increased mRNA for CD63 antigen in atherosclerotic lesions of
RT   Watanabe heritable hyperlipidemic rabbits.";
RL   Cell Struct. Funct. 19:219-225(1994).
CC   -!- FUNCTION: May play some role in signal transduction pathways.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D21264; BAA04804.1; -.
DR   PIR; JC2297; JC2297.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Antigen; Transmembrane; Lysosome.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DOMAIN        1     10       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     11     31       POTENTIAL.
FT   DOMAIN       32     50       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     51     69       POTENTIAL.
FT   DOMAIN       70     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    106       POTENTIAL.
FT   DOMAIN      107    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    203    223       POTENTIAL.
FT   DOMAIN      224    237       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    124    124       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   237 AA;  25498 MW;  063454D727E8A36C CRC64;

  Query Match             15.6%;  Score 255.5;  DB 1;  Length 237;
  Best Local Similarity   29.7%;  Pred. No. 6.8e-15;
  Matches   73;  Conservative   44;  Mismatches  108;  Indels   21;  Gaps    7;

Qy          2 AREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFP 61
              | |  :||:: ||| | | |  ':: ::||    :  |:  :|         |   :  |
Db          1 AVEGGMKCVKFLLYVLLLAFCACAVGLIAVGVGAQLVLSQTIT-------HGATPGSLLP 53

Qy         62 VVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMV 121
              |   :|||  || :|  :| ||| | |  |:  :   | :|  ||:|  :  |       |
Db         54 V---VIIAVGAFLFLVAFVGCCGTCKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDKV 110

Qy        122 PVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM--DWPPD 179
               :::     : :| ||        |    :  |::| |||   :|||  :  |  |  ||
Db        111 MSEFNK--DFRQQMQNYSTDNQTAL--ILDRMQKDFTCCGAANYTDWATIPGMTRDRVPD 166

Qy        180 SCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMI 239
              ||||    ||  :    :: |:| ||| :|:  :||  | : |:    : |   ::| ::
Db        167 SCCVNVTSGCGVKF---NVKDIYVEGCVEKIGLWLR--KNVLVVAAAALGIAFVEVLGIV 221

Qy        240 LTITLL 245
                 |:
Db        222 FACCLV 227


RESULT 10
CD63_HUMAN
ID   CD63_HUMAN     STANDARD;      PRT;   237 AA.
AC   P08962;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   CD63 antigen (Melanoma-associated antigen ME491) (Lysosome-associated
DE   membrane glycoprotein 3) (LAMP-3) (Ocular melanoma-associated
DE   antigen) (OMA81H) (Granulophysin).
GN   CD63 OR MLA1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88210273; PubMed=3365686;
RA   Hotta H., Ross A.H., Huebner K., Isobe M., Wendeborn S., Chao M.V.,
RA   Ricciardi R.P., Tsujimoto Y., Croce C.M., Koprowski H.;
RT   "Molecular cloning and characterization of an antigen associated with
RT   early stages of melanoma tumor progression.";
RL   Cancer Res. 48:2955-2962(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91131632; PubMed=1993697;
RA   Metzelaar M.J., Wijngaard P.L., Peters P.J., Sixma J.J.,
RA   Nieuwenhuis H.K., Clevers H.C.;
RT   "CD63 antigen. A novel lysosomal membrane glycoprotein, cloned by a
RT   screening procedure for intracellular antigens in eukaryotic cells.";
RL   J. Biol. Chem. 266:3239-3245(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=91025550; PubMed=2171551;
RA   Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,
RA   Scheit K.H.;
RT   "Characterization of three abundant mRNAs from human ovarian
RT   granulosa cells.";
RL   DNA Cell Biol. 9:479-485(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92287132; PubMed=1599482;
RA   Hotta H., Miyamoto H., Hara I., Takahashi N., Homma M.;
RT   "Genomic structure of the ME491/CD63 antigen gene and functional
RT   analysis of the 5'-flanking regulatory sequences.";
RL   Biochem. Biophys. Res. Commun. 185:436-442(1992).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92181348; PubMed=1339263;
RA   Wang M.X., Earley J.J. Jr., Shields J.A., Donoso L.A.;
RT   "An ocular melanoma-associated antigen. Molecular characterization.";
RL   Arch. Ophthalmol. 110:399-404(1992).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung, and Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 1-20.
RX   MEDLINE=86049405; PubMed=4062294;
RA   Ross A.H., Dietzschold B., Jackson D.M., Earley J.J., Ghrist B.F.D.,
RA   Atkinson B., Koprowski H.;
RT   "Isolation and amino terminal sequencing of a novel
RT   melanoma-associated antigen.";
RL   Arch. Biochem. Biophys. 242:540-548(1985).
RN   [8]
RP   CARBOHYDRATE-LINKAGE SITE ASN-129.
RX   MEDLINE=22660472; PubMed=12754519;
RA   Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT   "Identification and quantification of N-linked glycoproteins using
RT   hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL   Nat. Biotechnol. 21:660-666(2003).
CC   -!- FUNCTION: THIS ANTIGEN IS ASSOCIATED WITH EARLY STAGES OF MELANOMA
CC       TUMOR PROGRESSION. MAY PLAY A ROLE IN GROWTH REGULATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC   -!- TISSUE SPECIFICITY: DYSPLASTIC NEVI, RADIAL GROWTH PHASE PRIMARY
CC       MELANOMAS, HEMATOPOIETIC CELLS, TISSUE MACROPHAGES.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD63 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd63.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07982; CAA30792.1; -.
DR   EMBL; M58485; -; NOT_ANNOTATED_CDS.
DR   EMBL; M59907; AAA63235.1; -.
DR   EMBL; X62654; CAA44519.1; -.
DR   EMBL; S93788; AAB21617.1; -.
DR   EMBL; BC002349; AAH02349.1; -.
DR   EMBL; BC013017; AAH13017.1; -.
DR   PIR; I38016; I38016.
DR   Genew; HGNC:1692; CD63.
DR   MIM; 155740; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005765; C:lysosomal membrane; TAS.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Antigen; Transmembrane; Lysosome.
FT   INIT_MET      0      0
FT   DOMAIN        1     10       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     11     31       POTENTIAL.
FT   DOMAIN       32     50       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     51     69       POTENTIAL.
FT   DOMAIN       70     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    106       POTENTIAL.
FT   DOMAIN      107    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    203    223       POTENTIAL.
FT   DOMAIN      224    237       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   237 AA;  25505 MW;  0CBC38F831CF0C9B CRC64;

  Query Match             15.3%;  Score 250.5;  DB 1;  Length 237;
  Best Local Similarity   27.6%;  Pred. No. 1.8e-14;
  Matches   68;  Conservative   52;  Mismatches  105;  Indels   21;  Gaps    7;

Qy          2 AREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFP 61
              | |  :||:: ||| | | |   :: ::||             : ::| :: |   :  |
Db          1 AVEGGMKCVKFLLYVLLLAFCACAVGLIAVGV-------GAQLVLSQTIIQGATPGSLLP 53

Qy         62 VVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMV 121
              |   |:||| || :|  :| || | |  |:  :   | :|  ||:|  :  |     |
Db         54 V---VIIAVGVFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDKV 110

Qy        122 PVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM--DWPPD 179
                ::::    : :| ||  |:        :  | :|||||   :||| ::  |  :  ||
Db        111 MSEFNN--NFRQQMENY--PKNNHTASILDRMQADFKCCGAANYTDWEKIPSMSKNRVPD 166

Qy        180 SCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMI 239
              |||:    ||   :::   :::||| :|:  :||  | : |:    : |   ::| ::
Db        167 SCCINVTVGCGINFNEK---AIHKEGCVEKIGGWLR--KNVLVVAAAALGIAFVEVLGIV 221

Qy        240 LTITLL 245
                |:
Db        222 FACCLV 227


RESULT 11
CD63_BOVIN
ID   CD63_BOVIN     STANDARD;      PRT;   236 AA.
AC   Q9XSK2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   CD63 antigen.
GN   CD63.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=99328909; PubMed=10398809;
RA   Brooke G.P., Sopp P., Kwong L.S., Howard C.J.;
RT   "Molecular cloning of cattle CD63 and evidence for high level
RT   expression on subpopulations of dendritic cells.";
RL   Immunogenetics 49:812-814(1999).
CC   -!- FUNCTION: May play some role in signal transduction pathways.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ012589; CAB40564.1; -.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Antigen; Transmembrane; Lysosome.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DOMAIN        1     10       CYTOPLASMIC (POTENTIAL).
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FT   TRANSMEM     11     31       POTENTIAL.
FT   DOMAIN       32     50       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     51     69       POTENTIAL.
FT   DOMAIN       70     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    106       POTENTIAL.
FT   DOMAIN      107    201       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    202    222       POTENTIAL.
FT   DOMAIN      223    236       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     39     39       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   236 AA;  25648 MW;  91AF09A0B338CE09 CRC64;

  Query Match             14.9%;  Score 244;  DB 1;  Length 236;
  Best Local Similarity   29.0%;  Pred. No. 6.6e-14;
  Matches   71;  Conservative   46;  Mismatches  108;  Indels   20;  Gaps    7;

Qy          2 AREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFP 61
                | |  :||::  |||  |  |:|     :: ::||          ||   :|            |     |
Db          1 AVEGGMKCVKFLLYVLLLVFCACAVGLIAVGVGTHLVLNQTIT-------HGATPSFLLP 53

Qy         62 VVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMV 121
              |    |:|||  || :|   :|  ||   |   |   |:  :     |  :|   ||:|   :    |      |
Db         54 V---VIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDKV 110

Qy        122 PVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM-DWPPDS 180
               :::       : :|  ||   |:            :      |::|:|||     :|||  ::  :  :  |||
Db        111 RSEFNK--DFRQQMKNY--PKDNQTASILDKMQKDFECCGAANYTDWEKILAVTNKVPDS 166

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              |||         |             :  | ::  |||  :|:  ::||   |  |:     :      |    :|| ::|
Db        167 CCVNITHNCGINF---VVKDIHTEGCVEKIAAWLR--KNVLVVVAAALGIAFVEILGIVL 221

Qy        241 TITLL 245
                 |:
Db        222 ACCLV 226

RESULT 12
CD63_RAT
ID   CD63_RAT       STANDARD;      PRT;   237 AA.
AC   P28648;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   CD63 antigen (AD1 antigen).
GN   CD63.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92340890; PubMed=1634775;
RA   Nishikata H., Oliver C., Mergenhagen S.E., Siraganian R.P.;
RT   "The rat mast cell antigen AD1 (homologue to human CD63 or melanoma
RT   antigen ME491) is expressed in other cells in culture.";
RL   J. Immunol. 149:862-870(1992).
RN   [2]
RP   SEQUENCE OF 1-43.
RX   MEDLINE=91107696; PubMed=1703158;
RA   Kitani S., Berenstein E., Mergenhagen S.E., Tempst P.,
RA   Siraganian R.P.;
RT   "A cell surface glycoprotein of rat basophilic leukemia cells close
RT   to the high affinity IgE receptor (Fc epsilon RI). Similarity to
RT   human melanoma differentiation antigen ME491.";
RL   J. Biol. Chem. 266:1903-1909(1991).
CC   -!- FUNCTION: MAY BE INVOLVED IN THE SECRETORY PROCESS OF MAST CELLS
CC       AND MAY PLAY SOME ROLE IN SIGNAL TRANSDUCTION PATHWAYS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC       SECRETORY GRANULES AND PLASMA MEMBRANE OF MANY CULTURED CELL
CC       LINES.
CC   -!- TISSUE SPECIFICITY: ON MAST CELLS & PLATELETS OF RAT TISSUES.
CC       INDUCED IN OTHER CELLS IN CULTURE.
CC   -!- DEVELOPMENTAL STAGE: INCREASED EXPRESSION OF THE AD1 ANTIGEN IN
CC       EMBRYONAL TISSUES.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X61654; CAA43835.1; -.
DR   PIR; A46508; A46508.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Antigen; Transmembrane; Lysosome.
FT   INIT_MET      0      0
FT   DOMAIN        1     10       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     11     31       POTENTIAL.
FT   DOMAIN       32     50       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     51     69       POTENTIAL.
FT   DOMAIN       70     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    106       POTENTIAL.
FT   DOMAIN      107    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    203    223       POTENTIAL.
FT   DOMAIN      224    237       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   237 AA;  25567 MW;  3FE87E6DF3D72854 CRC64;

  Query Match             14.5%;  Score 237.5;  DB 1;  Length 237;
  Best Local Similarity   28.5%;  Pred. No. 2.4e-13;
  Matches   72;  Conservative   46;  Mismatches  100;  Indels   35;  Gaps    9;

Qy          2 AREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFP 61
                | |  :||::  |||  |  |  |     :: ::|:    ::    |    :|            |    :   |
Db          1 AVEGGMKCVKFLLYVLLLAFCACAVGLIAIGVAVQVVLKQAIT-------HETTAGSLLP 53

Qy         62 VVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMV 121
              |    |:|||  || :|   :|  ||   |   |   |:  :     |  :|   ||:|   :    |
Db         54 V---VIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAVAIAGYVFRDQV 110

Qy        122 PVQWSDMVTLKARMTNYGLPRYRWLTH-----AWNFFQREFKCCGVVYFTDWLEMTEM-- 174
               ::|     :  : :|  ||            ||          :   |:|  ||||    :|||   :    |
Db        111 KSEFSK--SFQKQMQNY-------LTDNKTATILDKLQKENKCCGASNYTDWERIPGMAK 161

Qy        175 DWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGV-- 232
               |  ||||:     ||        :       |  :: :||  :  :  ::||          ||    |  ::|:
Db        162 DRVPDSCCINITVGCGNDFKE---STIHTQGCVETIAAWLR----KNVLLVAGAALGIAF 214

Qy        233 TQILAMILTITLL 245
                ::|  :|  :   |:
Db        215 VEVLGIIFSCCLV 227

RESULT 13
CD82_HUMAN
ID   CD82_HUMAN     STANDARD;      PRT;   267 AA.
AC   P27701;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   CD82 antigen (Inducible membrane protein R2) (C33 antigen) (IA4)
DE   (Metastasis suppressor Kangai 1) (Suppressor of tumorigenicity-6).
GN   KAI1 OR CD82 OR SAR2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood lymphocytes;
RX   MEDLINE=91153380; PubMed=1842498;
RA   Gaugitsch H.W., Hofer E., Huber N.E., Schnabl E., Baumruker T.;
RT   "A new superfamily of lymphoid and melanoma cell proteins with
RT   extensive homology to Schistosoma mansoni antigen Sm23.";
RL   Eur. J. Immunol. 21:377-383(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93017900; PubMed=1401919;
RA   Imai T., Fukudome K., Takagi S., Nagira M., Furuse M., Fukuhara N.,
RA   Nishimura M., Hinuma Y., Yoshie O.;
RT   "C33 antigen recognized by monoclonal antibodies inhibitory to human
RT   T cell leukemia virus type 1-induced syncytium formation is a member
RT   of a new family of transmembrane proteins including CD9, CD37, CD53,
RT   and CD63.";
RL   J. Immunol. 149:2879-2886(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95273964; PubMed=7754374;
RA   Dong J.T., Barrett J.C.;
RT   "KAI1, a metastasis suppressor gene for prostate cancer on human
RT   chromosome 11p11.2.";
RL   Science 268:884-886(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Dong J.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ASSOCIATES WITH CD4 OR CD8 AND DELIVERS COSTIMULATORY
CC       SIGNALS FOR THE TCR/CD3 PATHWAY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: LYMPHOID SPECIFIC.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD82 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd82.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X53795; CAA37804.1; -.
DR   EMBL; S48196; AAB23825.1; -.
DR   EMBL; U20770; AAC50133.1; -.
DR   EMBL; U67274; AAC51205.1; -.
DR   EMBL; U67268; AAC51205.1; JOINED.
DR   EMBL; U67269; AAC51205.1; JOINED.
DR   EMBL; U67270; AAC51205.1; JOINED.
DR   EMBL; U67271; AAC51205.1; JOINED.
DR   EMBL; U67272; AAC51205.1; JOINED.
DR   EMBL; U67273; AAC51205.1; JOINED.
DR   PIR; I38942; A46493.
DR   Genew; HGNC:6210; KAI1.
DR   MIM; 600623; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Transmembrane; Antigen.
FT   DOMAIN        1     11       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      12    32       POTENTIAL.
FT   DOMAIN        33    53       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      54    72       POTENTIAL.
FT   DOMAIN        73    83       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      84    110      POTENTIAL.
FT   DOMAIN        111   228      EXTRACELLULAR (POTENTIAL)
FT   TRANSMEM      229   250      POTENTIAL.
FT   DOMAIN        251   267      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      157   157      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      198   198      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      240   241      II -> MV (IN REF. 2).
SQ   SEQUENCE   267 AA;  29625 MW;  FC379855BD1CABDE CRC64;

  Query Match           14.5%;  Score 237.5;  DB 1;  Length 267;
  Best Local Similarity   27.0%;  Pred. No. 2.7e-13;
  Matches   71;  Conservative   51;  Mismatches  100;  Indels   41;  Gaps   10;

Qy          7 VKCLRCLLYALNLLFWLMSISVLAVSAWM----RDYLNNVLTLTAETRVEEAVILTYFPV 62
              :|  :  |:  ||:|:::   :|    |:      ::: : | ::  |:       |
Db          6 IKVTKYFLFLFNLIFFILGAVILGFGVWILADKSSFISVLQTSSSSLRMG-----AY--- 57

Qy         63 VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVP 122
               | | |   :::| ||  | |     || ||  ||:|   ::  |   |     :
Db         58 ---VFIGVGAVTMLMGFLGCIGAVNEVRCLLGLYFAFLLLILIAQVTAGALFYFNMGKLK 114

Qy        123 VQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTE-MDWP---- 177
               :   :||   |  :|   |   |  ||:: | : |||| | | :|  :  | |: |
Db        115 QEMGGIVTELIR--DYNSSREDSLQDAWDYVQAQVKCCGWVSFYNWTDNAELMNRPEVTY 172

Qy        178 PDSCCVR-------------EFPGCSKQA--HQEDLSDLYQEGCGKKMYSFLRGTKQLQ 221
              | || |:             | ||   |:  | ||   :||||| :|: ::|:  : |
Db        173 PCSCEVKGEEDNSLSVRKGFCEAPGNRTQSGNHPEDW-PVYQEGCMEKVQAWLQ--ENLG 229

Qy        222 VLRFLGISIGVTQILAMILTITL 244
              ::  :|: : : ::| |:|:| |
Db        230 IILGVGVGVAIIELLGMVLSICL 252


RESULT 14
CD63_MOUSE
ID   CD63_MOUSE     STANDARD;      PRT;   237 AA.
AC   P41731;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   CD63 antigen.
GN   CD63.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94198294; PubMed=8148377;
RA   Miyamoto M., Homma M., Hotta H.;
RT   "Molecular cloning of the murine homologue of CD63/ME491 and
RT   detection of its strong expression in the kidney and activated
RT   macrophages.";
RL   Biochim. Biophys. Acta 1217:312-316(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y S N , Krzywinski M I , Skalska U , Smailus D.E.,
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RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May play some role in signal transduction pathways.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal.
CC   -!- TISSUE SPECIFICITY: Strongly expressed in kidney.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D16432; BAA03904.1; -.
DR   EMBL; BC008108; AAH08108.1; -.
DR   EMBL; BC012212; AAH12212.1; -.
DR   PIR; S43511; S43511.
DR   MGD; MGI:99529; Cd63.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Antigen; Transmembrane; Lysosome.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DOMAIN        1     10       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     11     31       POTENTIAL.
FT   DOMAIN       32     50       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     51     69       POTENTIAL.
FT   DOMAIN       70     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    106       POTENTIAL.
FT   DOMAIN      107    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    203    223       POTENTIAL.
FT   DOMAIN      224    237       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    115    115       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   237 AA;  25635 MW;  3C6EF16873B2A01C CRC64;

  Query Match             13.9%;  Score 227.5;  DB 1;  Length 237;
  Best Local Similarity   27.6%;  Pred. No. 1.7e-12;
  Matches   68;  Conservative   48;  Mismatches  109;  Indels   21;  Gaps    8;

Qy          2 AREDSVKCLRCLLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFP 61
              |  |  :||:: ||| | | |   :: ::|:   ::  |   :|         |    :  |
Db          1 AVEGGMKCVKFLLLYVLLLAFCACAVGLIAIGVAVQVVLKQAIT-------HETTAGSLLP 53

Qy         62 VVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMV 121
              |   |:|||  || :|  :| || | |  |: :   | :|  ||:|  :  |      |
Db         54 V---VIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAVAIAGYVFRDQV 110

Qy        122 PVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM--DWPPD 179
                :::   : : :| || |   :  |   :  |:|  |||   :|||  :  |  |  ||
Db        111 KSEFNK--SFQQQMQNY-LKDNKTAT-ILDKLQKENNCCGASNYTDWENIPGMAKDRVPD 166

Qy        180 SCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMI 239
              |||:    ||      :   | :: :|| : :  :||  | : ::   : |   ::| :|
Db        167 SCCINITVGCGNDFKE---STIHTQGCVETIAIWLR--KNILLVAAAALGIAFVEVLGII 221

Qy        240 LTITLL 245
               :  |:
Db        222 FSCCLV 227


RESULT 15
CD9_PIG
ID   CD9_PIG        STANDARD;      PRT;   225 AA.
AC   Q8WMQ3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   CD9 antigen.
GN   CD9.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yubero N., Barbancho M.J., Llanes D., Garrido J.J.;
RT   "Molecular cloning of the pig homolog of tetraspanin CD9 antigen.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN PLATELET ACTIVATION AND AGGREGATION (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AY072785; AAL68966.1; -.
DR   InterPro; IPR008952; Tetraspanin.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Glycoprotein; Antigen; Transmembrane; Lipoprotein.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DOMAIN        1     11       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     12     32       POTENTIAL.
FT   DOMAIN       33     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     73       POTENTIAL.
FT   DOMAIN       74     84       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     85    108       POTENTIAL.
FT   DOMAIN      109    192       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    193    218       POTENTIAL.
FT   DOMAIN      219    225       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     49     49       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   225 AA;  25070 MW;  FF280FE39BC11545 CRC64;

  Query Match             13.4%;  Score 220.5;  DB 1;  Length 225;
  Best Local Similarity   25.0%;  Pred. No. 6.5e-12;
  Matches   66;  Conservative   45;  Mismatches   86;  Indels   67;  Gaps    9;

Qy          8 KCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETR---VEEAVILTYFPVVH 64
              ||:: ||:  | :|||  |:|||:  |:|          ::|:    :|    :::  |:
Db          7 KCIKYLLFGFNFIFWLAGIAVLAIGLWLR--------FDSQTKSIFEQENNNSSFYTGVY 58

Qy         65 PVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ 124
               ::|    :::|| || || |: :  :|  :|| ||||| :|:|  :| |  :  |  :
Db         59 -ILIGAGALMMVVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDQVIKE 117

Qy        125 WSDMV---------------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDW 168
               |                  ||||   :| |                  |||::   :
Db        118 VQDFYRDTYNKLKGKDDPQRETLKA--IHYAL----------------DCCGLMGEVEQ 158

Qy        169 LEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGI 228
              |          | |  |:            || |  : | : :    :   :  ::  :||
Db        159 L-------LADICPQRDV----------LSSLPMKPCPEAIKEVFQ--NKFHIIGAVGI 198

Qy        229 SIGVTQILAMILTITLLWALYYDR 252
              | |  |  || :: |  |:   |
Db        199 GIAVVMIFGMIFSMILCCAIRRSR 222


Search completed: May 13, 2004, 16:06:11
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Job time : 12.3363 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:03:45 ; Search time 17.8142 Seconds
(without alignments)
883.899 Million cell updates/sec

Title: US-09-830-328C-2
Perfect score: 1642
Sequence: 1 MAREDSVKCLRCLLYALNLL.....IFEHTSMANSFNTHFEMEEL 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	286	17.4	253	3	US-09-333-599-4	Sequence 4, Appli
2	286	17.4	253	4	US-09-499-781-4	Sequence 4, Appli
3	280	17.1	253	3	US-09-333-599-2	Sequence 2, Appli
4	280	17.1	253	4	US-09-499-781-2	Sequence 2, Appli
5	268	16.3	236	3	US-08-705-771-19	Sequence 19, Appl
6	268	16.3	236	4	US-09-417-540-19	Sequence 19, Appl
7	242.5	14.8	280	2	US-08-855-140-1	Sequence 1, Appli
8	237.5	14.5	267	3	US-08-430-225A-20	Sequence 20, Appl
9	232.5	14.2	265	2	US-08-807-044-1	Sequence 1, Appli
10	215.5	13.1	228	1	US-08-408-222B-1	Sequence 1, Appli
11	214.5	13.1	227	1	US-08-254-493-1	Sequence 1, Appli
12	214.5	13.1	227	2	US-08-253-751-6	Sequence 6, Appli
13	214.5	13.1	227	2	US-08-453-925-6	Sequence 6, Appli
14	214.5	13.1	227	4	US-08-403-253A-6	Sequence 6, Appli
15	214.5	13.1	227	4	US-08-435-816A-6	Sequence 6, Appli
16	204	12.4	237	3	US-08-808-148-3	Sequence 3, Appli
17	204	12.4	237	4	US-09-976-594-216	Sequence 216, App
18	193.5	11.8	219	2	US-08-855-140-4	Sequence 4, Appli
19	176	10.7	204	4	US-09-149-476-429	Sequence 429, App
20	175.5	10.7	281	3	US-08-808-148-4	Sequence 4, Appli
21	174.5	10.6	219	2	US-08-855-140-3	Sequence 3, Appli
22	174.5	10.6	219	2	US-08-807-044-3	Sequence 3, Appli
23	174.5	10.6	219	5	PCT-US91-04986-2	Sequence 2, Appli
24	163.5	10.0	252	3	US-08-705-771-17	Sequence 17, Appl
25	163.5	10.0	252	4	US-09-417-540-17	Sequence 17, Appl
26	148.5	9.0	241	3	US-08-808-148-1	Sequence 1, Appli
27	148.5	9.0	241	3	US-09-020-956-114	Sequence 114, App
28	148.5	9.0	241	3	US-09-030-607-114	Sequence 114, App
29	148.5	9.0	241	4	US-09-439-313-114	Sequence 114, App
30	148.5	9.0	241	4	US-09-352-616A-114	Sequence 114, App
31	148.5	9.0	241	4	US-09-232-149A-114	Sequence 114, App
32	148.5	9.0	241	4	US-09-159-812-114	Sequence 114, App
33	148.5	9.0	241	4	US-09-636-215-114	Sequence 114, App
34	148.5	9.0	241	4	US-09-685-166A-114	Sequence 114, App
35	148.5	9.0	241	4	US-09-115-453-114	Sequence 114, App
36	148.5	9.0	241	4	US-09-688-489-114	Sequence 114, App
37	148.5	9.0	260	3	US-08-957-130-15	Sequence 15, Appl
38	145.5	8.9	233	4	US-09-148-545-137	Sequence 137, App
39	142	8.6	245	4	US-09-482-273-133	Sequence 133, App
40	123	7.5	258	3	US-08-957-130-13	Sequence 13, Appl
41	98.5	6.0	123	4	US-09-149-476-693	Sequence 693, App
42	98.5	6.0	336	4	US-09-716-129-62	Sequence 62, Appl
43	90	5.5	418	1	US-08-194-338-9	Sequence 9, Appli
44	89	5.4	417	3	US-08-430-286A-12	Sequence 12, Appl
45	89	5.4	417	5	PCT-US91-00909-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-333-599-4
; Sequence 4, Application US/09333599
; Patent No. 6245898
; GENERAL INFORMATION:
; APPLICANT: Testa, Jacqueline E.
; APPLICANT: Quigley, James P.
; APPLICANT: Seandel, Marco
; TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
; TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
; FILE REFERENCE: SUNY
; CURRENT APPLICATION NUMBER: US/09/333,599
; CURRENT FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-333-599-4

Query Match 17.4%; Score 286; DB 3; Length 253;
Best Local Similarity 28.8%; Pred. No. 2.3e-22;
Matches 74; Conservative 47; Mismatches 96; Indels 40; Gaps 9;

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Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| | :        ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASS--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDM 128
                 ::: |:|| | | |    ||  ||  ||:|| :|:  |:  |  : ::  :
Db         66 VAGVVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYVYQQLLNTE---- 121

Qy        129 VTLKARMTNYGLPRYRWLTH-----AWNFFQREFKCCGVVYFTDWLEMTEMDW------- 176
               ||  : :  : ||    |      |: :  |:|| |||      ||    : :|
Db        122 --LKENLKDTMVKRYHQSGHEGVSSAVDKLQQEFHCCGSNNSQDW---QDSEWIRSGEAD 176

Qy        177 ---PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIG 231
                 |||||     || |: |    |::|  : ||  |: :|::  : |:|:  :|| |
Db        177 SRVVPDSCCKTMVAGCGKRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIA 231

Qy        232 VTQILAMILTITLLWAL 248
               |:  || |  |  :|
Db        232 CVQVFGMIFTCCLYRSL 248
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RESULT 2
US-09-499-781-4
; Sequence 4, Application US/09499781
; Patent No. 6498014

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; GENERAL INFORMATION:
;  APPLICANT:  Testa, Jacqueline E.
;  APPLICANT:  Quigley, James P.
;  APPLICANT:  Seandel, Marco
;  TITLE OF INVENTION:  MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
;  TITLE OF INVENTION:  ASSOCIATED WITH TUMOR METASTASIS
;  FILE REFERENCE:  SUNY
;  CURRENT APPLICATION NUMBER: US/09/499,781
;  CURRENT FILING DATE:  2000-02-08
;  PRIOR APPLICATION NUMBER:  09/333,599
;  PRIOR FILING DATE:  1999-06-15
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-499-781-4

  Query Match             17.4%;  Score 286;  DB 4;  Length 253;
  Best Local Similarity   28.8%;  Pred. No. 2.3e-22;
  Matches   74;  Conservative   47;  Mismatches   96;  Indels   40;  Gaps    9;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| | :        ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASS--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDM 128
                 ::: |:|| | | |    ||  ||  ||:|| :|:  |:  |  : ::  :
Db         66 VAGVVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYVYQQLLNTE---- 121

Qy        129 VTLKARMTNYGLPRYRWLTH-----AWNFFQREFKCCGVVYFTDWLEMTEMDW------- 176
               ||  : :  : ||    |     | :  |:|| |||     ||    : :|
Db        122 --LKENLKDTMVKRYHQSGHEGVSSAVDKLQQEFHCCGSNNSQDW---QDSEWIRSGEAD 176

Qy        177 ---PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIG 231
                  |||||     || |: |    |::|  : ||  |: :|::  : |:|:  :|| |
Db        177 SRVVPDSCCKTMVAGCGKRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIA 231

Qy        232 VTQILAMILTITLLWAL 248
                |:  || |  |  :|
Db        232 CVQVFGMIFTCCLYRSL 248


RESULT 3
US-09-333-599-2
; Sequence 2, Application US/09333599
; Patent No. 6245898
; GENERAL INFORMATION:
;  APPLICANT: Testa, Jacqueline E.
;  APPLICANT: Quigley, James P.
;  APPLICANT: Seandel, Marco
;  TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
;  TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
;  FILE REFERENCE: SUNY
;  CURRENT APPLICATION NUMBER: US/09/333,599
;  CURRENT FILING DATE: 1999-06-15
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-333-599-2

  Query Match             17.1%;  Score 280;  DB 3;  Length 253;
  Best Local Similarity   29.8%;  Pred. No. 1e-21;
  Matches   76;  Conservative   46;  Mismatches   97;  Indels   36;  Gaps   10;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| |          ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASG--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWS 126
                 ::: |:|| | | |    ||  ||  ||:|| :|:  |:  :  | |:|   ::
Db         66 VAGTVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYAYYQQLNTELK-- 123

Qy        127 DMVTLKARMT-NYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW--------- 176
                 ||  ||  |  | :  :| | :  |:|| |||     ||    : :|
Db        124 --ENLKDTMTKRYHQPGHEAVTSAVDQLQQEFHCCGSNNSQDW---RDSEWIRSQEAGGR 178

Qy        177 -PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIGVT 233
                |||||       | :: |    |::|  : ||  |: :|::  : |:|:  :|| |
Db        179 VVPDSCCKTVVALCGQRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIACV 233

Qy        234 QILAMILTITLLWAL 248
                |:  || |  |  :|
Db        234 QVFGMIFTCCLYRSL 248


RESULT 4
US-09-499-781-2
; Sequence 2, Application US/09499781
; Patent No. 6498014
; GENERAL INFORMATION:
;  APPLICANT:  Testa, Jacqueline E.
;  APPLICANT:  Quigley, James P.
;  APPLICANT:  Seandel, Marco
;  TITLE OF INVENTION:  MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
;  TITLE OF INVENTION:  ASSOCIATED WITH TUMOR METASTASIS
;  FILE REFERENCE:  SUNY
;  CURRENT APPLICATION NUMBER: US/09/499,781
;  CURRENT FILING DATE:  2000-02-08
;  PRIOR APPLICATION NUMBER:  09/333,599
;  PRIOR FILING DATE:  1999-06-15
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-499-781-2

  Query Match             17.1%;  Score 280;  DB 4;  Length 253;
  Best Local Similarity   29.8%;  Pred. No. 1e-21;
  Matches   76;  Conservative   46;  Mismatches   97;  Indels   36;  Gaps   10;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| |          ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASG--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWS 126
                 ::: |:|| | | |    ||  ||  ||:|| :|:  |:  :  | |:|   ::
Db         66 VAGTVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYAYYQQLNTELK-- 123

Qy        127 DMVTLKARMT-NYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW--------- 176
                 ||  ||  |  | :  :| | :  |:|| |||     ||    : :|
Db        124 --ENLKDTMTKRYHQPGHEAVTSAVDQLQQEFHCCGSNNSQDW---RDSEWIRSQEAGGR 178

Qy        177 -PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIGVT 233
                |||||       | :: |    |::|  : ||  |: :|::  : |:|:  :|| |
Db        179 VVPDSCCKTVVALCGQRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIACV 233

Qy        234 QILAMILTITLLWAL 248
                |:  || |  |  :|
Db        234 QVFGMIFTCCLYRSL 248


RESULT 5
US-08-705-771-19
; Sequence 19, Application US/08705771
; Patent No. 6054289
;  GENERAL INFORMATION:
;    APPLICANT:  Paul Moore, Reiner Gentz, Hongjin Ji,
;    APPLICANT:  Jian Ni and Jing-Shan Hu
;    TITLE OF INVENTION·  Human Genes, Sequences and
```

```
;    TITLE OF INVENTION:  Expression Products
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/705,771
;      FILING DATE:  August 30, 1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-346 (PF196)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  973-994-1700
;      TELEFAX:  973-994-1744
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  236 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-705-771-19

  Query Match             16.3%;  Score 268;  DB 3;  Length 236;
  Best Local Similarity   27.0%;  Pred. No. 1.8e-20;
  Matches   70;  Conservative   45;  Mismatches   98;  Indels   46;  Gaps    7;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |||    :: :: |::| ||||||     || |   |:      :   ||::         |
Db          1 MARA-CLQAVKYLMFAFNLLFWLGGCGVLGVGIWLAAQQGSFATLSSS-----------F 48

Qy         61 PVVHP--VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVE--LACGVWTYE 116
              | :    ::|    |:: :| :|  | :| |  ||  :|  ||::| :|  :|   : |
Db         49 PSLWAANLLIITGAFVMAIGFVGCLGAIKENKCLLLTFFLLLLLVFLLEGTIAILFFAYT 108

Qy        117 QELMVPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW 176
               ::     |       ||  :  ||       ||:||:  | :|:|||| :||| |:
Db        109 DKIDRYAQQD----LKKGLHLYGTQGNVGLTNAWSIIQTDFRCCGVSNYTDWFEVYNATR 164

Qy        177 PPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRG---------TKQLQVLRFLG 227
              |||||:                 : | ||    : : |         : :|  :   |
Db        165 VPDSCCLE-----------------FSESCGLHAPALVEGRATRGEGVASGELLAVGIFG 207

Qy        228 ISIGVTQILAMILTITLLW 246
              :   : ||| :   :|: |
Db        208 LCTALVQILGLNFAMTMYW 226


RESULT 6
US-09-417-540-19
; Sequence 19, Application US/09417540
; Patent No. 6639052
;  GENERAL INFORMATION:
;      APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
;                 Jian Ni and Jing-Shan Hu
;      TITLE OF INVENTION: Human Genes, Sequences and
;                          Expression Products
;      NUMBER OF SEQUENCES: 22
;      CORRESPONDENCE ADDRESS:
;           ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                      CECCHI, STEWART & OLSTEIN
;           STREET: 6 BECKER FARM ROAD
;           CITY: ROSELAND
;           STATE: NEW JERSEY
;           COUNTRY: USA
;           ZIP: 07068
;      COMPUTER READABLE FORM:
;           MEDIUM TYPE: 3.5 INCH DISKETTE
;           COMPUTER: IBM PS/2
;           OPERATING SYSTEM: MS-DOS
;           SOFTWARE: WORD PERFECT 5.1
;      CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/417,540
;           FILING DATE: 14-Oct-1999
;           CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/705,771
;           FILING DATE: August 30, 1996
;      ATTORNEY/AGENT INFORMATION:
;           NAME: MULLINS, J.G.
;           REGISTRATION NUMBER: 33,073
;           REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
;      TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 973-994-1700
;           TELEFAX: 973-994-1744
;  INFORMATION FOR SEQ ID NO: 19:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 236 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-417-540-19

  Query Match             16.3%;  Score 268;  DB 4;  Length 236;
  Best Local Similarity   27.0%;  Pred. No. 1.8e-20;
  Matches   70;  Conservative   45;  Mismatches   98;  Indels   46;  Gaps    7;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |||    :: :: |::| ||||||     || |   |:      :   ||::         |
Db          1 MARA-CLQAVKYLMFAFNLLFWLGGCGVLGVGIWLAAQQGSFATLSSS-----------F 48

Qy         61 PVVHP--VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVE--LACGVWTYE 116
              | :    ::|    |:: :| :|  | :| |  ||  :|  ||::| :|  :|   : |
Db         49 PSLWAANLLIITGAFVMAIGFVGCLGAIKENKCLLLTFFLLLLLVFLLEGTIAILFFAYT 108

Qy        117 QELMVPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW 176
               ::     |       ||  :  ||       ||:||:  | :|:|||| :||| |:
Db        109 DKIDRYAQQD----LKKGLHLYGTQGNVGLTNAWSIIQTDFRCCGVSNYTDWFEVYNATR 164

Qy        177 PPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRG---------TKQLQVLRFLG 227
              |||||:                 : | ||    : : |         : :|  :   |
Db        165 VPDSCCLE-----------------FSESCGLHAPALVEGRATRGEGVASGELLAVGIFG 207

Qy        228 ISIGVTQILAMILTITLLW 246
              :   : ||| :   :|: |
Db        208 LCTALVQILGLNFAMTMYW 226


RESULT 7
US-08-855-140-1
; Sequence 1, Application US/08855140
; Patent No. 5854022
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Guegler, Karl J.
;    TITLE OF INVENTION:  NEW TRANSMEMBRANE PROTEIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
```

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;       COUNTRY:  USA
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/855,140
;       FILING DATE:  Herewith
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0296 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  280 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       LIBRARY:  MYOMNOT01
;       CLONE:  779308
US-08-855-140-1

  Query Match             14.8%;  Score 242.5;  DB 2;  Length 280;
  Best Local Similarity   27.4%;  Pred. No. 1.2e-17;
  Matches   61;  Conservative   35;  Mismatches   90;  Indels   37;  Gaps    6;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHP--V 66
              ||: :::  ||:|||    :| |  |:      |  | :                ||  :    :
Db          8 CLKYMMFLFNLIFWLCGCGLLGVGIWLSVSQGNFATFSPS-----------FPSLSAANL 56

Qy         67 MIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPV--- 123
              :||:   :::  |  ||  | :|  |  ||  :|  |||          |  ||::|:
Db         57 VIAIGTIVMVTGFLGCLGAIKENKCLLLSFFIVLLV-----------TLLAELILPILFF 105

Qy        124 QWSDMVT------LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWP 177
               :  |  |        ||  :  |       | :|||  |  | :||||  :|||  :   :
Db        106 VYMDKVNENAKKDLKEGLLLYHTENNVGLKNAWNIIQAEMRCCGVTDYTDWYPVLGENTV 165

Qy        178 PDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQL 220
              || ||:    ||  :       : |:: ||  |:  :    | :
Db        166 PDRCCMENSQGCGRNG----TTPLWRTGCXXKVKMWFDDNKHV 204


RESULT 8
US-08-430-225A-20
; Sequence 20, Application US/08430225A
; Patent No. 6204000
;  GENERAL INFORMATION:
;    APPLICANT:  Dong, Jin-Tang; Barrett,
;    APPLICANT:  J. Carl; Lamb, Patricia W.; Isaacs, John T.
;    TITLE OF INVENTION:  DIAGNOSTIC METHODS AND
;    TITLE OF INVENTION:  GENE THERAPY USING REAGENTS DERIVED FROM THE
;    TITLE OF INVENTION:  HUMAN METASTASIS SUPPRESSOR GENE KAI1
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,225A
;      FILING DATE:  28-APR-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RICHARD W. BORK
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4172
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;      TELEX:  421792
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
US-08-430-225A-20

  Query Match             14.5%;  Score 237.5;  DB 3;  Length 267;
  Best Local Similarity   27.0%;  Pred. No. 3.8e-17;
  Matches   71;  Conservative   51;  Mismatches  100;  Indels   41;  Gaps   10;

Qy          7 VKCLRCLLYALNLLFWLMSISVLAVSAWM----RDYLNNVLTLTAETRVEEAVILTYFPV 62
              :|  :  |:  ||:|:::   :|    |:       ::: : | ::  |:       |
Db          6 IKVTKYFLFLFNLIFFILGAVILGFGVWILADKSSFISVLQTSSSSLRMG-----AY--- 57

Qy         63 VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVP 122
                | |  |    :::| ||  | |      ||  ||  ||:|   ::  |   |     :
Db         58 ---VFIGVGAVTMLMGFLGCIGAVNEVRCLLGLYFAFLLLILIAQVTAGALFYFNMGKLK 114

Qy        123 VQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTE-MDWP---- 177
               :  :||   |  :|   |   |  ||:: | : |||| | | :| :  | |: |
Db        115 QEMGGIVTELIR--DYNSSREDSLQDAWDYVQAQVKCCGWVSFYNWTDNAELMNRPEVTY 172

Qy        178 PDSCCVR--------------EFPGCSKQA--HQEDLSDLYQEGCGKKMYSFLRGTKQLQ 221
              | || |:              | ||   |:  | ||   :|||| :|: ::|:  : |
Db        173 PCSCEVKGEEDNSLSVRKGFCEAPGNRTQSGNHPEDW-PVYQEGCMEKVQAWLQ--ENLG 229

Qy        222 VLRFLGISIGVTQILAMILTITL 244
              ::  :|: : : ::|  |:|:| |
Db        230 IILGVGVGVAIIELLGMVLSICL 252


RESULT 9
US-08-807-044-1
; Sequence 1, Application US/08807044
; Patent No. 5863735
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/807,044
;      FILING DATE:  Herewith
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;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0224 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  SCORNOT01
;      CLONE:  663655
US-08-807-044-1

  Query Match             14.2%;  Score 232.5;  DB 2;  Length 265;
  Best Local Similarity   24.4%;  Pred. No. 1.3e-16;
  Matches   68;  Conservative   47;  Mismatches  103;  Indels   61;  Gaps    8;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |||   :: :: |::| ||||||    || |  |:           | |:   |   : |
Db          1 MARA-CLQAVKYLMFAFNLLFWLGGCGVLGVGIWL----------AATQGSFATXSSSF 48

Qy         61 PVVHP--VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQE 118
              | :    ::|    |:: :| :|  | :| |  ||  :|  ||::| :|    :  :
Db         49 PSLSAANLLIITGAFVMAIGFVGCLGAIKENKCLLLTFFLLLLLVFLLEATIAILFF--- 105

Qy        119 LMVPVQWSDMV------TLKARMTNYGLPRYRWLTHAWNFFQR---------------- 155
                 ::| :       ||  :  ||       ||:||:  |
Db        106 -----AYTDKIDRYAQQDLKKGLHLYGTQGNVGLTNAWSIIQTDXRGVGRWAGSAGAPSP 160

Qy        156 ----------EFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEG 205
                      :|:|||| :||| |:      |||||:     |   |          ::
Db        161 XASARPELAPQFRCCGVSNYTDWFEVYNATRVPDSCCLEFSESCGLHAP----GTWWKAP 216

Qy        206 CGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITL 244
              | : :  :|: : |  :   |:   : ||| :   :|:
Db        217 CYETVKVWLQ--ENLLAVGIFGLCTALVQILGLTFAMTM 253


RESULT 10
US-08-408-222B-1
; Sequence 1, Application US/08408222B
; Patent No. 5776727
;  GENERAL INFORMATION:
;    APPLICANT:  Ikeyama, Shuichi
;    APPLICANT:  Koyama, Masaru
;    APPLICANT:  Miyake, Masauyki
;    APPLICANT:  Senoo, Masaharu
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY, POLYPEPTIDES AND
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dike, Bronstein, Roberts & Cushman
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/408,222B
;      FILING DATE:  22-MAR-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/254,493
;      FILING DATE:  06-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP-079996-1991
;      FILING DATE:  12-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP-085396-1991
;      FILING DATE:  14-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP-022321-1992
;      FILING DATE:  07-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  41777-DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
US-08-408-222B-1

  Query Match             13.1%;  Score 215.5;  DB 1;  Length 228;
  Best Local Similarity   24.5%;  Pred. No. 6.7e-15;
  Matches   67;  Conservative   44;  Mismatches   93;  Indels   69;  Gaps   10;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |  :   ||:: ||:  | :|||  |:|||:  |:|           ||    :  :::
Db          1 MPVKGGTKCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNNNS---SFY 57

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY--EQE 118
               |: ::|     :::|| || || |: :  :|  :|| ||||| :|:|  :| |  : |
Db         58 TGVY-ILIGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDE 116

Qy        119 LMVPVQ--WSDMV-----------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVY 164
              ::  ||  : |                |||   :| |                 |||:
Db        117 VIKEVQEFYKDTYNKLKTKDEPQRETLKA--IHYAL-----------------NCCGL-- 155

Qy        165 FTDWLEMTEMDWPP-----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQ 219
                :|    |  |      ::  |:  |    |:                        :
Db        156 -AGGVEQFISDICPKKDVLETFTVKSCPDAIKEVFD----------------------NK 192

Qy        220 LQVLRFLGISIGVTQILAMILTITLLWALYYDR 252
              ::  :|| | |  |  || :: | :|:  :|
Db        193 FHIIGAVGIGIAVVMIFGMIFSMILCCAIRRNR 225


RESULT 11
US-08-254-493-1
; Sequence 1, Application US/08254493
; Patent No. 5439886
;  GENERAL INFORMATION:
;    APPLICANT:  IKEYAMA, SHUICHI
;    APPLICANT:  KOYAMA, MASARU
;    APPLICANT:  MIYAKE, MASAYUKI
;    APPLICANT:  SENOO, MASAHARU
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY, POLYPEPTIDES AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
```

```
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/254,493
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/865552
;      FILING DATE:  09-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 079996-1991
;      FILING DATE:  12-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 085396-1991
;      FILING DATE:  17-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 022321-1992
;      FILING DATE:  07-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RESNICK, DAVID S.
;      REGISTRATION NUMBER:  34235
;      REFERENCE/DOCKET NUMBER:  41777
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  227 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-254-493-1

  Query Match             13.1%;  Score 214.5;  DB 1;  Length 227;
  Best Local Similarity   24.8%;  Pred. No. 8.5e-15;
  Matches   66;  Conservative   43;  Mismatches   88;  Indels   69;  Gaps   10;

Qy          8 KCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVM 67
              ||:: ||:  | :|||  |:|||:  |:|           ||    :   :::  |: ::
Db          7 KCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNNNS---SFYTGVY-IL 62

Qy         68 IAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY--EQELMVPVQ- 124
                  :::|| || || |: :  :|  :|| ||||| :|:|  :| |  : |::  ||
Db         63 IGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDEVIKEVQE 122

Qy        125 -WSDMV------------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEM 171
               : |              ||||   :| |                  |||:      :|
Db        123 FYKDTYNKLKTKDEPQRETLKA--IHYAL----------------NCCGL---AGGVEQ 160

Qy        172 TEMDWPP-----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFL 226
                  |  |     ::  |:  |   |:                          :  ::  :
Db        161 FISDICPKKDVLETFTVKSCPDAIKEVFD--------------------NKFHIIGAV 198

Qy        227 GISIGVTQILAMILTITLLWALYYDR 252
              || | |  |  || :: |  |:  :|
Db        199 GIGIAVVMIFGMIFSMILCCAIRRNR 224


RESULT 12
US-08-253-751-6
; Sequence 6, Application US/08253751
; Patent No. 5858358
;  GENERAL INFORMATION
;    APPLICANT:  June, Carl H.
;    APPLICANT:  Thompson, Craig B.
;    APPLICANT:  Nabel, Gary J.
;    APPLICANT:  Gray, Gary S.
;    APPLICANT:  Rennert, Paul D.
;    APPLICANT:  Freeman, Gordon J.
;    TITLE OF INVENTION:  METHODS FOR SELECTIVELY STIMULATING
;    TITLE OF INVENTION:  PROLIFERATION OF T-CELLS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,751
;      FILING DATE:  3 JUNE 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/073,223
;      FILING DATE:  4 JUNE 1993
;      APPLICATION NUMBER:  US 08/200,947
;      FILING DATE:  23 FEB 1994
;      APPLICATION NUMBER:  US 07/864,805
;      FILING DATE:  7 APR 1992
;      APPLICATION NUMBER:  US 08/247,505
;      FILING DATE:  23 MAY 1994
;      APPLICATION NUMBER:  US 07/864,866
;      FILING DATE:  7 APR 1992
;      APPLICATION NUMBER:  08/218,155
;      FILING DATE:  25 MAR 1994
;      APPLICATION NUMBER:  US 07/864,807
;      FILING DATE:  7 APR 1992
;      APPLICATION NUMBER:  US 07/902,467
;      FILING DATE:  16 JUNE 1992
;      APPLICATION NUMBER:  US 07/275,433
;      FILING DATE:  23 NOV 1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  RPI-002CPB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  227 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-253-751-6

  Query Match             13.1%;  Score 214.5;  DB 2;  Length 227;
  Best Local Similarity   24.8%;  Pred. No. 8.5e-15;
  Matches   66;  Conservative   43;  Mismatches   88;  Indels   69;  Gaps   10;

Qy          8 KCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVM 67
              ||:: ||:  | :|||  |:|||:  |:|           ||    :   :::  |: ::
Db          7 KCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNNNS---SFYTGVY-IL 62

Qy         68 IAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY--EQELMVPVQ- 124
                  :::|| || || |: :  :|  :|| ||||| :|:|  :| |  : |::  ||
Db         63 IGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDEVIKEVQE 122

Qy        125 -WSDMV------------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEM 171
               : |              ||||   :| |                  |||:      :|
Db        123 FYKDTYNKLKTKDEPQRETLKA--IHYAL----------------NCCGL---AGGVEQ 160
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Qy        172 TEMDWPP-----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFL 226
              |  |      ::  |:  |   |:                                :  ::  :
Db        161 FISDICPKKDVLETFTVKSCPDAIKEVFD---------------------NKFHIIGAV 198

Qy        227 GISIGVTQILAMILTITLLWALYYDR 252
              || | |  |  || :: |  |:  :|
Db        199 GIGIAVVMIFGMIFSMILCCAIRRNR 224
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RESULT 13
US-08-453-925-6
; Sequence 6, Application US/08453925
; Patent No. 5883223
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,925
; FILING DATE: 30 MAY 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,751
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-925-6

Query Match 13.1%; Score 214.5; DB 2; Length 227;
Best Local Similarity 24.8%; Pred. No. 8.5e-15;
Matches 66; Conservative 43; Mismatches 88; Indels 69; Gaps 10;

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Qy          8 KCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVM 67
              ||:: ||:  | :|||  |:|||:  |:|           ||    :   :::  |: ::
Db          7 KCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNNNS---SFYTGVY-IL 62

Qy         68 IAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY--EQELMVPVQ- 124
              |      :::|| || || |: :  :|  :|| ||||| :|:|  :| |  : |::  ||
Db         63 IGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDEVIKEVQE 122

Qy        125 -WSDMV-----------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEM 171
               : |              ||||   :| |                 |||:      :|
Db        123 FYKDTYNKLKTKDEPQRETLKA--IHYAL----------------NCCGL---AGGVEQ 160

Qy        172 TEMDWPP-----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFL 226
              |  |      ::  |:  |   |:                                :  ::  :
Db        161 FISDICPKKDVLETFTVKSCPDAIKEVFD---------------------NKFHIIGAV 198

Qy        227 GISIGVTQILAMILTITLLWALYYDR 252
              || | |  |  || :: |  |:  :|
Db        199 GIGIAVVMIFGMIFSMILCCAIRRNR 224
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RESULT 14
US-08-403-253A-6
; Sequence 6, Application US/08403253A
; Patent No. 6352694
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,253A
; FILING DATE: March 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 742-4214
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  227 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-403-253A-6

  Query Match           13.1%;  Score 214.5;  DB 4;  Length 227;
  Best Local Similarity  24.8%;  Pred. No. 8.5e-15;
  Matches   66;  Conservative   43;  Mismatches   88;  Indels   69;  Gaps   10;

Qy          8 KCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVM 67
              ||:: ||:  | :|||  |:|||:  |:|          ||    :   ::: |: ::
Db          7 KCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNNNS---SFYTGVY-IL 62

Qy         68 IAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY--EQELMVPVQ- 124
                |     :::|| || || |: :  :|  :|| ||||| :|:|  :| |  : |::  ||
Db         63 IGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDEVIKEVQE 122

Qy        125 -WSDMV------------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEM 171
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Db        123 FYKDTYNKLKTKDEPQRETLKA--IHYAL----------------NCCGL---AGGVEQ 160

Qy        172 TEMDWPP-----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFL 226
                | |      ::  |:  |   |:                          :  ::  :
Db        161 FISDICPKKDVLETFTVKSCPDAIKEVFD--------------------NKFHIIGAV 198

Qy        227 GISIGVTQILAMILTITLLWALYYDR 252
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Db        199 GIGIAVVMIFGMIFSMILCCAIRRNR 224


RESULT 15
US-08-435-816A-6
; Sequence 6, Application US/08435816A
; Patent No. 6534055
;  GENERAL INFORMATION:
;    APPLICANT:  June, Carl H.
;    APPLICANT:  Thompson, Craig B.
;    APPLICANT:  Nabel, Gary J.
;    APPLICANT:  Gray, Gary S.
;    APPLICANT:  Rennert, Paul D.
;    TITLE OF INVENTION:  Methods For Selectively Stimulating Proliferation Of T-Cells
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,816A
;      FILING DATE:  May 4, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/403,253
;      FILING DATE:  10 MARCH 1995
;      APPLICATION NUMBER:  US 08/253,964
;      FILING DATE:  3 JUNE 1994
;      APPLICATION NUMBER:  US 08/073,223
;      FILING DATE:  4 JUNE 1993
;      APPLICATION NUMBER:  US 08/200,947
;      FILING DATE:  23 FEB 1994
;      APPLICATION NUMBER:  US 07/864,805
;      FILING DATE:  7 APR 1992
;      APPLICATION NUMBER:  US 08/247,505
;      FILING DATE:  23 MAY 1994
;      APPLICATION NUMBER:  US 07/864,866
;      FILING DATE:  7 APR 1992
;      APPLICATION NUMBER:  US 08/218,155
;      FILING DATE:  25 MAR 1994
;      APPLICATION NUMBER:  US 07/864,807
;      FILING DATE:  7 APR 1992
;      APPLICATION NUMBER:  US 07/902,467
;      FILING DATE:  16 JUNE 1992
;      APPLICATION NUMBER:  US 07/275,433
;      FILING DATE:  23 NOV 1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  RPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  227 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-435-816A-6

  Query Match           13.1%;  Score 214.5;  DB 4;  Length 227;
  Best Local Similarity  24.8%;  Pred. No. 8.5e-15;
  Matches   66;  Conservative   43;  Mismatches   88;  Indels   69;  Gaps   10;

Qy          8 KCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVM 67
              ||:: ||:  | :|||  |:|||:  |:|          ||    :   ::: |: ::
Db          7 KCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNNNS---SFYTGVY-IL 62

Qy         68 IAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY--EQELMVPVQ- 124
                |     :::|| || || |: :  :|  :|| ||||| :|:|  :| |  : |::  ||
Db         63 IGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDEVIKEVQE 122

Qy        125 -WSDMV------------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEM 171
               : |               ||||   :| |                 |||:      :|
Db        123 FYKDTYNKLKTKDEPQRETLKA--IHYAL----------------NCCGL---AGGVEQ 160

Qy        172 TEMDWPP-----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFL 226
                | |      ::  |:  |   |:                          :  ::  :
Db        161 FISDICPKKDVLETFTVKSCPDAIKEVFD--------------------NKFHIIGAV 198

Qy        227 GISIGVTQILAMILTITLLWALYYDR 252
              || | |  |  || ::  |  |:  :|
Db        199 GIGIAVVMIFGMIFSMILCCAIRRNR 224


Search completed: May 13, 2004, 16:09:02
Job time : 18.8142 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:02:15 ; Search time 14.5752 Seconds
(without alignments)
2012.897 Million cell updates/sec

Title: US-09-830-328C-2
Perfect score: 1642
Sequence: 1 MAREDSVKCLRCLLYALNLL.....IFEHTSMANSFNTHFEMEEL 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	260.5	15.9	238	1	JC2297	CD63 antigen - rab
2	259	15.8	238	2	A59265	tetraspan TSPAN-4
3	255.5	15.6	238	1	I38016	melanoma-associate
4	242.5	14.8	238	1	A46508	CD63/ME491 antigen
5	237.5	14.5	267	1	A46493	metastasis suppres
6	232.5	14.2	238	1	S43511	CD63/ME491 antigen
7	220	13.4	206	2	T25161	hypothetical prote
8	215.5	13.1	228	1	A40402	CD9 antigen [valid
9	214.5	13.1	226	1	JX0221	CD9 antigen - bovi
10	213.5	13.0	228	1	A42929	CD9 antigen - gree
11	212.5	12.9	226	2	I49589	antigen - mouse
12	211.5	12.9	226	1	S39262	CD9 antigen - rat
13	204	12.4	237	1	A36056	tumor-associated a
14	199	12.1	236	1	A35649	cell surface prote
15	193	11.8	236	1	A46472	cell surface prote
16	192.5	11.7	281	1	A47629	cell surface glyco
17	191	11.6	244	1	I39368	T-cell acute lymph
18	187	11.4	245	2	A59258	tetraspan TSPAN-6
19	184.5	11.2	219	1	A39574	leukocyte antigen
20	184	11.2	253	2	A59264	tetraspan TSPAN-3
21	182.5	11.1	282	2	T21696	hypothetical prote
22	180	11.0	222	2	A59263	tetraspan TSPAN-2
23	178	10.8	245	2	A59260	tetraspan TSPAN-6
24	175	10.7	266	2	I49561	C33/R2/IA4 - mouse
25	174.5	10.6	219	1	A37243	hemopoietic cell s
26	171.5	10.4	281	1	B47629	cell surface glyco
27	164.5	10.0	218	1	A43522	23K integral membr
28	162	9.9	264	2	A59261	tetraspan TSPAN-5
29	158	9.6	359	2	T18667	hypothetical prote
30	148.5	9.0	260	2	I46081	uroplakin Ib - bov
31	145.5	8.9	218	1	A40181	23K integral membr
32	145	8.8	321	2	T45053	hypothetical prote
33	144.5	8.8	241	2	A59262	tetraspan TSPAN-1
34	144	8.8	308	2	T24912	hypothetical prote
35	139	8.5	210	2	I58391	sarcoma amplified
36	138	8.4	427	2	T32652	hypothetical prote
37	137.5	8.4	244	2	T13615	hypothetical prote
38	128	7.8	260	2	A41531	TGFbeta-regulated
39	126	7.7	223	2	T26763	hypothetical prote
40	123	7.5	258	2	I46080	uroplakin Ia - bov
41	122	7.4	702	2	T34313	hypothetical prote
42	117.5	7.2	194	2	T25548	hypothetical prote
43	114.5	7.0	374	2	T15940	hypothetical prote
44	110.5	6.7	366	2	T22544	hypothetical prote
45	109	6.6	242	2	T15361	hypothetical prote

ALIGNMENTS

RESULT 1
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CD63 antigen - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C;Accession: JC2297
R;Sohma, Y.; Suzuki, T.; Sasano, H.; Nagura, H.; Nose, M.; Yamamoto, T.
Cell Struct. Funct. 19, 219-225, 1994
A;Title: Increased mRNA for CD63 antigen in atherosclerotic lesions of Watanable heritab
A;Reference number: JC2297; MUID:95120837; PMID:7820873
A;Accession: JC2297
A;Molecule type: mRNA
A;Residues: 1-238 <SOH>
A;Cross-references: DDBJ:D21264; NID:g684973; PIDN:BAA04804.1; PID:g684974
A;Experimental source: aorta
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F;1-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-51/Domain: extracellular #status predicted <EX1>
F;52-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-202/Domain: extracellular #status predicted <EX2>
F;203-228/Domain: transmembrane #status predicted <TM4>
F;229-238/Domain: intracellular #status predicted <CY3>
F;125,130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.9%; Score 260.5; DB 1; Length 238;
Best Local Similarity 30.0%; Pred. No. 3.3e-16;
Matches 74; Conservative 44; Mismatches 108; Indels 21; Gaps 7;

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Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
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Db          1 MAVEGGMKCVKFLLYVLLLAFCACAVGLIAVGVGAQLVLSQTIT-------HGATPGSLL 53

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||   |:||| || :|  :| ||| | |  |:  :   | :|  ||:|  :  |
Db         54 PV---VIIAVGAFLFLVAFVGCCGTCKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDK 110

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM--DWPP 178
              |  :::     : :| ||        |     :  |::| |||   :|||  :  |  |  |
Db        111 VMSEFNK--DFRQQMQNYSTDNQTAL--ILDRMQKDFTCCGAANYTDWATIPGMTRDRVP 166

Qy        179 DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAM 238
              |||||    ||  :    :: |:| ||| :|:  :||  | : |:    : |   ::| :
Db        167 DSCCVNVTSGCGVKF---NVKDIYVEGCVEKIGLWLR--KNVLVVAAAALGIAFVEVLGI 221

Qy        239 ILTITLL 245
              :   |:
Db        222 VFACCLV 228
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RESULT 2
A59265
tetraspan TSPAN-4 - human
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 02-Jun-2000
C;Accession: A59265
R;Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A;Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
A;Reference number: A59258; MUID:98390278; PMID:9714763
A;Accession: A59265
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-238 <TOD>
A;Cross-references: GB:AF054841; NID:g2997746; PIDN:AAC69717.1; PID:g2997747
C;Genetics:
A;Gene: TSPAN-4
C;Superfamily: CD9 antigen

Query Match 15.8%; Score 259; DB 2; Length 238;
Best Local Similarity 27.0%; Pred. No. 4.5e-16;
Matches 68; Conservative 48; Mismatches 102; Indels 34; Gaps 7;

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Db          1 MARA-CLQAVKYLMFAFNLLFWLGGCGVLGVGIWL----------AATQGSFATLSSSF 48

Qy         61 PVVHP--VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQE 118
                 :    ::|    |:: :| :|  | :| |  ||  :|  ||::| :|    :  :
Db         49 PSLSAANLLIITGAFVMAIGFVGCLGAIKENKCLLLTFFLLLLLVFLLEATIAILFF--- 105

Qy        119 LMVPVQWSDMV------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMT 172
                 ::| :       ||  :  ||       ||:||:  | :|:|||  :||| |:
Db        106 -----AYTDKIDRYAQQDLKKGLHLYGTQGNVGLTNAWSIIQTDFRCCGVSNYTDWFEVY 160

Qy        173 EMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGV 232
                |||||:      |  |       ::  | : :  :|:  : |  :    |:  :
Db        161 NATRVPDSCCLEFSESCGLHAP----GTWWKAPCYETVKVWLQ--ENLLAVGIFGLCTAL 214

Qy        233 TQILAMILTITL 244
               ||| :   :|:
Db        215 VQILGLTFAMTM 226
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RESULT 3
I38016
melanoma-associated antigen CD63 [validated] - human
N;Alternate names: antigen ME491; lysosomal membrane glycoprotein CD63; ME491/CD63 antig
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 09-Aug-1996 #text_change 08-Dec-2000
C;Accession: I38016; S01418; A39514; B35826; A61177; A61173; A56782
R;Hotta, H.; Miyamoto, H.; Hara, I.; Takahashi, N.; Homma, M.
Biochem. Biophys. Res. Commun. 185, 436-442, 1992
A;Title: Genomic structure of the ME491/CD63 antigen gene and functional analysis of the
A;Reference number: I38016; MUID:92287132; PMID:1599482
A;Accession: I38016
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-238 <RES>
A;Cross-references: EMBL:X62654; NID:g430755; PIDN:CAA44519.1; PID:g430756
R;Hotta, H.; Ross, A.H.; Huebner, K.; Isobe, M.; Wendeborn, S.; Chao, M.V.; Ricciardi, R
Cancer Res. 48, 2955-2962, 1988
A;Title: Molecular cloning and characterization of an antigen associated with early stag
A;Reference number: S01418; MUID:88210273; PMID:3365686
A;Accession: S01418
A;Molecule type: mRNA
A;Residues: 1-238 <HOT>
A;Cross-references: EMBL:X07982; NID:g34526; PIDN:CAA30792.1; PID:g34527
R;Metzelaar, M.J.; Wijngaard, P.L.J.; Peters, P.J.; Sixma, J.J.; Nieuwenhuis, H.K.; Clev
J. Biol. Chem. 266, 3239-3245, 1991
A;Title: CD63 antigen. A novel lysosomal membrane glycoprotein, cloned by a screening pr
A;Reference number: A39514; MUID:91131632; PMID:1993697
A;Accession: A39514
A;Molecule type: mRNA
A;Residues: 1-238 <MET>
A;Cross-references: GB:M58485
R;Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K.
DNA Cell Biol. 9, 479-485, 1990
A;Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.
A;Reference number: A35826; MUID:91025550; PMID:2171551
A;Accession: B35826
A;Molecule type: mRNA
A;Residues: 1-238 <RAP>
A;Cross-references: GB:M59907; NID:g189383; PIDN:AAA63235.1; PID:g189384
A;Note: the authors did not translate the codons for residues 205 through 224
R;Azorsa, D.O.; Hyman, J.A.; Hildreth, J.E.K.
Blood 78, 280-284, 1991
A;Title: CD63/Pltgp40: a platelet activation antigen identical to the stage-specific, mel
A;Reference number: A61177; MUID:91300080; PMID:2070066
A;Accession: A61177
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 2-68,'P',70-238 <AZO>
R;Hildreth, J.E.K.; Derr, D.; Azorsa, D.O.
Blood 77, 121-132, 1991
A;Title: Characterization of a novel self-associating Mr 40,000 platelet glycoprotein.
A;Reference number: A61173; MUID:91084576; PMID:1984792
A;Accession: A61173
A;Molecule type: protein
A;Residues: 2-8,'X',10-16,'XX',19-21 <HIL>
R;Wang, M.X.; Earley Jr., J.J.; Shields, J.A.; Donoso, L.A.
Arch. Ophthalmol. 110, 399-404, 1992
A;Title: An ocular melanoma-associated antigen. Molecular characterization.
A;Reference number: A56782; MUID:92181348; PMID:1339263
A;Accession: A56782
A;Molecule type: mRNA
A;Residues: 1-238 <WAN>
A;Cross-references: GB:S93788; NID:g246538; PIDN:AAB21617.1; PID:g246539
A;Experimental source: uveal melanoma
A;Note: sequence extracted from NCBI backbone (NCBIN:93788, NCBIP:93790)
C;Genetics:
A;Gene: GDB:CD63; MLA1
A;Cross-references: GDB:120186; OMIM:155740
A;Map position: 12q12-12q13
A;Introns: 22/3; 85/3; 110/3; 142/3; 189/3; 217/3
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F;2-238/Product: melanoma-associated antigen ME491 #status experimental <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-51/Domain: extracellular #status predicted <EX1>
F;52-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-202/Domain: extracellular #status predicted <EX2>
F;203-228/Domain: transmembrane #status predicted <TM4>
F;229-238/Domain: intracellular #status predicted <CY3>
F;130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.6%; Score 255.5; DB 1; Length 238;
Best Local Similarity 27.9%; Pred. No. 9.4e-16;
Matches 69; Conservative 52; Mismatches 105; Indels 21; Gaps 7;

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Qy          1 MAREDSVKCLRCLLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
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Db          1 MAVEGGMKCVKFLLYVLLLAFCACAVGLIAVGV-------GAQLVLSQTIIQGATPGSLL 53

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
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Db         54 PV---VIIAVGVFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDK 110

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM--DWPP 178
              |  ::::    : :| ||  |:        :  | :|||||   :||| ::  |  :  |
Db        111 VMSEFNN--NFRQQMENY--PKNNHTASILDRMQADFKCCGAANYTDWEKIPSMSKNRVP 166
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Qy        179 DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAM 238
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Db        167 DSCCINVTVGCGINFNEK---AIHKEGCVEKIGGWLR--KNVLVVAAAALGIAFVEVLGI 221

Qy        239 ILTITLL 245
              :   |:
Db        222 VFACCLV 228


RESULT 4
A46508
CD63/ME491 antigen homolog - rat
N;Alternate names: mast cell antigen AD1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: A46508; S16776
R;Nishikata, H.; Oliver, C.; Mergenhagen, S.E.; Siraganian, R.P.
J. Immunol. 149, 862-870, 1992
A;Title: The rat mast cell antigen AD1 (homologue to human CD63 or melanoma antigen ME49
A;Reference number: A46508; MUID:92340890; PMID:1634775
A;Accession: A46508
A;Molecule type: mRNA
A;Residues: 1-238 <NIS>
A;Cross-references: EMBL:X61654; NID:g55601; PIDN:CAA43835.1; PID:g55602
A;Note: this antigen was found localized to mast cells in tissue samples, but was induce
A;Note: sequence extracted from NCBI backbone (NCBIN:109346, NCBIP:109349)
C;Comment: This heavily glycosylated protein of 50-60K (27K after deglycosylation) is fo
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lysosome; mast cell; surface antigen; transmembrane protein
F;1-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-51/Domain: extracellular #status predicted <EX1>
F;52-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-202/Domain: extracellular #status predicted <EX2>
F;203-228/Domain: transmembrane #status predicted <TM4>
F;229-238/Domain: intracellular #status predicted <CY3>
F;130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           14.8%;  Score 242.5;  DB 1;  Length 238;
  Best Local Similarity  28.7%;  Pred. No. 1.4e-14;
  Matches   73;  Conservative   46;  Mismatches  100;  Indels   35;  Gaps    9;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||  |  :||:: ||| | | |   :: ::|:   ::   |   :|        |    :
Db          1 MAVEGGMKCVKFLLYVLLLAFCACAVGLIAIGVAVQVVLKQAIT-------HETTAGSLL 53

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||   |:|||  || :|  :| ||  | |  |:  :   | :|  ||:| :  |
Db         54 PV---VIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAVAIAGYVFRDQ 110

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTH-----AWNFFQREFKCCGVVYFTDWLEMTEM- 174
              |  ::|   : : :| ||        ||          :  |:| ||||   :|||  :  |
Db        111 VKSEFSK--SFQKQMQNY-------LTDNKTATILDKLQKENKCCGASNYTDWERIPGMA 161

Qy        175 -DWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGV- 232
               |  |||||:    ||      :   | :: :|| : : ::||      ||    | ::|:
Db        162 KDRVPDSCCINITVGCGNDFKE---STIHTQGCVETIAAWLR----KNVLLVAGAALGIA 214

Qy        233 -TQILAMILTITLL 245
               ::| :| :  |:
Db        215 FVEVLGIIFSCCLV 228


RESULT 5
A46493
metastasis suppressor KAI1 - human
N;Alternate names: cell surface glycoprotein KAI1; membrane protein R2, inducible; type
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: I38942; S16156; A46493
R;Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, J
Science 268, 884-886, 1995
A;Title: KAI1, a metastasis suppressor gene for prostate cancer on human chromosome 11p1
A;Reference number: I38942; MUID:95273964; PMID:7754374
A;Accession: I38942
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-267 <RES>
A;Cross-references: EMBL:U20770; NID:g806805; PIDN:AAC50133.1; PID:g806806
R;Gaugitsch, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.
Eur. J. Immunol. 21, 377-383, 1991
A;Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homolog
A;Reference number: S16156; MUID:91153380; PMID:1842498
A;Accession: S16156
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-267 <GAU>
A;Cross-references: EMBL:X53795; NID:g35832; PIDN:CAA37804.1; PID:g35833
A;Note: the authors translated the codon AGC for residue 50 as Thr
R;Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukuhara, N.; Nishimura, N
J. Immunol. 149, 2879-2886, 1992
A;Title: C33 antigen recognized by monoclonal antibodies inhibitory to human T cell leul
D9, CD37, CD53, and CD63.
A;Reference number: A46493; MUID:93017900; PMID:1401919
A;Accession: A46493
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-239,'MV',242-267 <IMA>
A;Cross-references: GB:S48196; NID:g258294; PIDN:AAB23825.1; PID:g258295
A;Experimental source: T-cell line MOLT-4
A;Note: sequence extracted from NCBI backbone (NCBIP:117149)
C;Genetics:
A;Gene: GDB:KAI1
A;Cross-references: GDB:134216; OMIM:600623
A;Map position: 11p11.2-11p11.2
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <CY1>
F;11-36/Domain: transmembrane #status predicted <TM1>
F;37-57/Domain: extracellular #status predicted <EX1>
F;58-78/Domain: transmembrane #status predicted <TM2>
F;79-83/Domain: intracellular #status predicted <CY2>
F;84-108/Domain: transmembrane #status predicted <TM3>
F;109-227/Domain: extracellular #status predicted <EX2>
F;228-252/Domain: transmembrane #status predicted <TM4>
F;253-265/Domain: intracellular #status predicted <CY3>
F;129,157,198/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           14.5%;  Score 237.5;  DB 1;  Length 267;
  Best Local Similarity  27.0%;  Pred. No. 4.6e-14;
  Matches   71;  Conservative   51;  Mismatches  100;  Indels   41;  Gaps   10;

Qy          7 VKCLRCLLYALNLLFWLMSISVLAVSAWM----RDYLNNVLTLTAETRVEEAVILTYFPV 62
              :|  :  |:  ||:|:::   :|    |:      ::: : | ::  |:       |
Db          6 IKVTKYFLFLFNLIFFILGAVILGFGVWILADKSSFISVLQTSSSSLRMG-----AY--- 57

Qy         63 VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVP 122
                | |  |   :::| ||  | |     ||  ||  ||:|   ::  |   |     :
Db         58 ---VFIGVGAVTMLMGFLGCIGAVNEVRCLLGLYFAFLLLILIAQVTAGALFYFNMGKLK 114

Qy        123 VQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTE-MDWP---- 177
               :   :||   |  :|   |   |  ||:: | : ||||  | | :| :  | |: |
Db        115 QEMGGIVTELIR--DYNSSREDSLQDAWDYVQAQVKCCGWVSFYNWTDNAELMNRPEVTY 172

Qy        178 PDSCCVR-------------EFPGCSKQA--HQEDLSDLYQEGCGKKMYSFLRGTKQLQ 221
              | || |:              | ||   |:  | ||   :|||| :|: ::|:  : |
Db        173 PCSCEVKGEEDNSLSVRKGFCEAPGNRTQSGNHPEDW-PVYQEGCMEKVQAWLQ--ENLG 229

Qy        222 VLRFLGISIGVTQILAMILTITL 244
              ::  :|: : : ::| |:|:| |
Db        230 IILGVGVGVAIIELLGMVLSICL 252


RESULT 6
```

```
S43511
CD63/ME491 antigen homolog - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C;Accession: S43511
R;Miyamoto, H.; Homma, M.; Hotta, H.
Biochim. Biophys. Acta 1217, 312-316, 1994
A;Title: Molecular cloning of the murine homologue of CD63/ME491 and detection of its st
A;Reference number: S43511; MUID:94198294; PMID:8148377
A;Accession: S43511
A;Molecule type: mRNA
A;Residues: 1-238 <MIY>
A;Cross-references: EMBL:D16432; NID:g484052; PIDN:BAA03904.1; PID:g976238
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F;1-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-51/Domain: extracellular #status predicted <EX1>
F;52-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-202/Domain: extracellular #status predicted <EX2>
F;203-228/Domain: transmembrane #status predicted <TM4>
F;229-238/Domain: intracellular #status predicted <CY3>
F;116,130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           14.2%;  Score 232.5;  DB 1;  Length 238;
  Best Local Similarity  27.9%;  Pred. No. 1.2e-13;
  Matches   69;  Conservative   48;  Mismatches  109;  Indels   21;  Gaps    8;

Qy          1 MAREDSVKCLRCLLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||  |  :||:: ||| | | |   :: ::|:   ::  |   :|          |   :
Db          1 MAVEGGMKCVKFLLYVLLLAFCACAVGLIAIGVAVQVVLKQAIT-------HETTAGSLL 53

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||   |:|||  || :|  :| ||  | |  |:  :   | :|  ||:|  :  |
Db         54 PV---VIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAVAIAGYVFRDQ 110

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM--DWPP 178
              |  :::   : : :| || |   :  |   :  |:|  |||   :|||  :  |  | | |
Db        111 VKSEFNK--SFQQQMQNY-LKDNKTAT-ILDKLQKENNCCGASNYTDWENIPGMAKDRVP 166

Qy        179 DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAM 238
              ||||:    ||     :   | :: :|| : :  :||  | : ::    : |   ::| :
Db        167 DSCCINITVGCGNDFKE---STIHTQGCVETIAIWLR--KNILLVAAAALGIAFVEVLGI 221

Qy        239 ILTITLL 245
              | :  |:
Db        222 IFSCCLV 228


RESULT 7
T25161
hypothetical protein T23D8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T25161
R;Wild, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19989
A;Accession: T25161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <WIL>
A;Cross-references: EMBL:Z81128; PIDN:CAB03397.1; GSPDB:GN00019; CESP:T23D8.2
A;Experimental source: clone T23D8
C;Genetics:
A;Gene: CESP:T23D8.2
A;Map position: 1
A;Introns: 21/3; 49/2; 93/3; 114/3; 163/1
C;Superfamily: CD9 antigen

  Query Match           13.4%;  Score 220;  DB 2;  Length 206;
  Best Local Similarity  25.9%;  Pred. No. 1.4e-12;
  Matches   64;  Conservative   47;  Mismatches   74;  Indels   62;  Gaps   10;

Qy          4 EDSVKCLRCLLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVV 63
              |  |  :: ||:  ||: |:  :|:: | : ::   :||| :  : |:   ::|
Db          3 EGGVTIVKYLLFLANLVLWVGGLSLIIVGSILQLKFDNVLDILGDERLATPILL------ 56

Qy         64 HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPV 123
                ::|   | |:  | || || :: |           | | | | ||
Db         57 --LVIGSLCTLL--GFLGCCGAIRENY--------CLTVSFAVLLAL------------ 91

Qy        124 QWSDMVTLKARMTNYGLPRY---RWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
                ::|          |: ||   | :  ||:   : |:||||   :|||  | :   |||
Db         92 ----LIT--------GMVRYHESRGVESAWDKTHQLFECCGVTNSSDWLTFTTI---PDS 136

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||: |  ||:::      : |:: ||       :   :|  ||:   :  |:  :|| |
Db        137 CCIEEIEGCAREN-----APLFEPGC-------IHSVEQ-WVLKNGAMVGGICAVLAAIQ 183

Qy        241 TITLLWA 247
                : : :|
Db        184 LVGVCFA 190


RESULT 8
A40402
CD9 antigen [validated] - human
N;Alternate names: motility-related protein-1
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1991 #sequence_revision 07-Jul-1995 #text_change 08-Dec-2000
C;Accession: A46123; A40402; JH0555; A39029; S10564
R;Rubinstein, E.; Benoit, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouchei
Genomics 16, 132-138, 1993
A;Title: Organization of the human CD9 gene.
A;Reference number: A46123; MUID:93252369; PMID:8486348
A;Accession: A46123
A;Molecule type: DNA
A;Residues: 1-228 <RUB>
A;Cross-references: GB:S60489; NID:g300112; PIDN:AAC60586.1; PID:g300115
A;Experimental source: leukocyte
A;Note: sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328,
R;Lanza, F.; Wolf, D.; Fox, C.F.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.;
J. Biol. Chem. 266, 10638-10645, 1991
A;Title: cDNA cloning and expression of platelet p24/CD9. Evidence for a new family of m
A;Reference number: A40402; MUID:91244846; PMID:2037603
A;Accession: A40402
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-228 <LAN>
A;Cross-references: GB:L34068; GB:M61880; NID:g508495; PIDN:AAA59982.1; PID:g508496
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Miyake, M.; Koyama, M.; Seno, M.; Ikeyama, S.
J. Exp. Med. 174, 1347-1354, 1991
A;Title: Identification of the motility-related protein (MRP-1), recognized by monoclona
A;Reference number: JH0555; MUID:92078843; PMID:1720807
A;Accession: JH0555
A;Molecule type: mRNA
A;Residues: 1-228 <MIY>
A;Cross-references: GB:X60111; NID:g34768; PIDN:CAA42708.1; PID:g34769
A;Experimental source: breast carcinoma
A;Note: this protein has the epitope defined by cell motility-inhibiting monoclonal anti
R;Boucheix, C.; Benoit, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uza
J. Biol. Chem. 266, 117-122, 1991
A;Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.
A;Reference number: A39029; MUID:91093112; PMID:1840589
A;Accession: A39029
A;Molecule type: mRNA
A;Residues: 1-8,'S',10-66,'A',68-193,195-228 <BOU>
A;Cross-references: GB:M38690
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.; Kurokawa, K.
FEBS Lett. 264, 270-274, 1990
A;Title: Purification and partial characterization of CD9 antigen of human platelets.
```

```
A;Reference number: S10564; MUID:90292223; PMID:2358073
A;Accession: S10564
A;Molecule type: protein
A;Residues: 2-8,'X',10-21 <HIG>
C;Genetics:
A;Gene: GDB:CD9; MIC3
A;Cross-references: GDB:120582; OMIM:143030
A;Map position: 12p13-12p13
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-228/Product: CD9 antigen #status experimental <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-55/Domain: extracellular #status predicted <EX1>
F;56-82/Domain: transmembrane #status predicted <TM2>
F;83-86/Domain: intracellular #status predicted <CY2>
F;87-111/Domain: transmembrane #status predicted <TM3>
F;112-194/Domain: extracellular #status predicted <EX2>
F;195-221/Domain: transmembrane #status predicted <TM4>
F;222-228/Domain: intracellular #status predicted <CY3>
F;53/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             13.1%;  Score 215.5;  DB 1;  Length 228;
  Best Local Similarity   24.5%;  Pred. No. 3.9e-12;
  Matches   67;  Conservative   44;  Mismatches   93;  Indels   69;  Gaps   10;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |  :   ||:: ||:  | :|||  |:|||:  |:|          ||    :   :::
Db          1 MPVKGGTKCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNNNS---SFY 57

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY--EQE 118
              |: ::|     :::|| || || |: :  :|  :|| ||||| :|:|  :| |  : |
Db         58 TGVY-ILIGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDE 116

Qy        119 LMVPVQ--WSDMV------------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVY 164
              ::  ||  : |               ||||   :| |                  |||:
Db        117 VIKEVQEFYKDTYNKLKTKDEPQRETLKA--IHYAL-----------------NCCGL-- 155

Qy        165 FTDWLEMTEMDWPP-----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQ 219
              :|   |  |      ::  |:  |   |:                        :
Db        156 -AGGVEQFISDICPKKDVLETFTVKSCPDAIKEVFD---------------------NK 192

Qy        220 LQVLRFLGISIGVTQILAMILTITLLWALYYDR 252
              ::  :|| | |  |  || :: |  |:  :|
Db        193 FHIIGAVGIGIAVVMIFGMIFSMILCCAIRRNR 225


RESULT 9
JX0221
CD9 antigen - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: JX0221
R;Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A;Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cell
A;Reference number: JX0221; MUID:93054422; PMID:1339429
A;Accession: JX0221
A;Molecule type: mRNA
A;Residues: 1-226 <MAR>
A;Cross-references: GB:M81720; NID:g162820; PIDN:AAA30439.1; PID:g162821
A;Experimental source: ocular ciliary epithelial cell
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-226/Product: CD9 antigen #status predicted <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-53/Domain: extracellular #status predicted <EX1>
F;54-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-109/Domain: transmembrane #status predicted <TM3>
F;110-192/Domain: extracellular #status predicted <EX2>
F;193-219/Domain: transmembrane #status predicted <TM4>
F;220-226/Domain: intracellular #status predicted <CY3>
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             13.1%;  Score 214.5;  DB 1;  Length 226;
  Best Local Similarity   24.3%;  Pred. No. 4.7e-12;
  Matches   67;  Conservative   51;  Mismatches   81;  Indels   77;  Gaps   13;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETR---VEEAVIL 57
              |  :   ||:: ||:  | :|||  |:||:|  |:|          ::|:   :|
Db          1 MPVKGGTKCIKYLLFGFNFIFWLAGIAVLSVGLWLR--------FDSQTKSIFEQENNDS 52

Qy         58 TYFPVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY-- 115
              :::  |: ::|     :::|| || || |: :  :|  :|  |||||  :|:|  :| |
Db         53 SFYTGVY-ILIGAGALMMLVGFLGCCGAVQESQCMLGLFFSFLLVIFAIEVAAAIWGYSH 111

Qy        116 EQELMVPVQ--WSDMVTLKARMTNYGLPRYRWLTHAWNFFQRE--------FKCCGVV-- 163
              ::|::  ||  : |       :: |    |             |||            |||:
Db        112 KEEVIKEVQKFYEDTYN---KLKNKDEP-----------QRETLKAIHIALDCCGLTGV 156

Qy        164 ---YFTDWLEMTEMDWPP----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRG 216
                 : ||          ||    ||   |  |          | : ::::
Db        157 PEQFLTD-------TCPPKNLIDSLKTRPCP--------EAIDEIFR------------- 188

Qy        217 TKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR 252
                :  ::  :|| | |  |  |: :: |  |:  :|
Db        189 -SKFHIIGAVGIGIAVVMIFGMVFSMILCCAIRRNR 223


RESULT 10
A42929
CD9 antigen - green monkey
N;Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C;Accession: A42929
R;Mitamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A;Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
eptors on toxin-sensitive cells.
A;Reference number: A42929; MUID:92394967; PMID:1522113
A;Accession: A42929
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-228 <MIT>
A;Cross-references: GB:D10726; NID:g218565; PIDN:BAA01569.1; PID:g218566
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-228/Product: CD9 antigen #status predicted <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-55/Domain: extracellular #status predicted <EX1>
F;56-82/Domain: transmembrane #status predicted <TM2>
F;83-86/Domain: intracellular #status predicted <CY2>
F;87-111/Domain: transmembrane #status predicted <TM3>
F;112-194/Domain: extracellular #status predicted <EX2>
F;195-221/Domain: transmembrane #status predicted <TM4>
F;222-228/Domain: intracellular #status predicted <CY3>
F;52,53/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             13.0%;  Score 213.5;  DB 1;  Length 228;
  Best Local Similarity   24.2%;  Pred. No. 5.9e-12;
  Matches   66;  Conservative   45;  Mismatches   93;  Indels   69;  Gaps   10;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |  :   ||:: ||:  | :|||  |:|||:  |:|          ||    :   :::
Db          1 MPVKGGTKCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQETNNNNS---SFY 57

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTY--EQE 118
              |: ::|     :::|| || || |: :  :|  :|| ||||| :|:|  :| |  : |
Db         58 TGVY-ILIGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAIWGYSHKDE 116

Qy        119 LMVPVQ--WSDMV------------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVY 164
              ::  ||  : |               ||||   :| |                  |||:
```

```
Db        117 VIKEVQEFYKDTYNKLKTKDEPQRETLKA--IHYAL-----------------DCCGL-- 155

Qy        165 FTDWLEMTEMDWPP-----DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQ 219
                :|    | |      ::  ::  |   |:          :
Db        156 -AGGVEQFISDICPKKDVLETFTIKSCPDAIKEVFD----------------------NK 192

Qy        220 LQVLRFLGISIGVTQILAMILTITLLWALYYDR 252
              ::  :|| | |  |  || :: |  |:  :|
Db        193 FHIIGAVGIGIAVVMIFGMIFSMILCCAIRRNR 225


RESULT 11
I49589
antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C;Accession: I49589
R;Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A;Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A;Reference number: I49589; MUID:94054345; PMID:8236164
A;Accession: I49589
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-226 <RES>
A;Cross-references: GB:L08115; NID:g388911; PIDN:AAA37405.1; PID:g388912
C;Superfamily: CD9 antigen

  Query Match             12.9%;  Score 212.5;  DB 2;  Length 226;
  Best Local Similarity   24.6%;  Pred. No. 7.2e-12;
  Matches   65;  Conservative   46;  Mismatches   86;  Indels   67;  Gaps   10;

Qy          8 KCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETR---VEEAVILTYFPVVH 64
              ||:: ||:  | :|||  |:|||:  |:|          ::|:    :|    :::  |:
Db          8 KCIKYLLFGFNFIFWLAGIAVLAIGLWLR--------FDSQTKSIFEQENNHSSFYTGVY 59

Qy         65 PVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVW--TYEQELMVP 122
               ::|     :::|| || || |: :  :|  :|| ||||| :|:|  ||  |:: |::
Db         60 -ILIGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAVWGYTHKDEVIKE 118

Qy        123 VQ--WSDMV------------TLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDW 168
              :|  : |                |||                          |||:
Db        119 LQEFYKDTYQKLRSKDEPQRETLKA------------------IHMALDCCGI---AGP 156

Qy        169 LEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGI 228
              ||    |  |    :  |     :  | :|:::                : ::  :||
Db        157 LEQFISDTCPKKQLLESF---QVKPCPEAISEVF--------------NNKFHIIGAVGI 199

Qy        229 SIGVTQILAMILTITLLWALYYDR 252
              | |  |  || :: |  |:   |
Db        200 GIAVVMIFGMIFSMILCCAIRRSR 223


RESULT 12
S39262
CD9 antigen - rat
N;Alternate names: platelet cell surface glycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: I56562; S39262
R;Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.
J. Neurosci. 15, 562-573, 1995
A;Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expre
A;Reference number: I56562; MUID:95123481; PMID:7823164
A;Accession: I56562
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-226 <RES>
A;Cross-references: EMBL:X76489; NID:g434314; PIDN:CAA54027.1; PID:g434315
C;Genetics:
A;Gene: CD9
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-53/Domain: extracellular #status predicted <EX1>
F;54-80/Domain: transmembrane #status predicted <TM2>
F;81-84/Domain: intracellular #status predicted <CY2>
F;85-109/Domain: transmembrane #status predicted <TM3>
F;110-192/Domain: extracellular #status predicted <EX2>
F;193-219/Domain: transmembrane #status predicted <TM4>
F;220-226/Domain: intracellular #status predicted <CY3>
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             12.9%;  Score 211.5;  DB 1;  Length 226;
  Best Local Similarity   25.4%;  Pred. No. 8.9e-12;
  Matches   64;  Conservative   46;  Mismatches   99;  Indels   43;  Gaps   10;

Qy          8 KCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETR---VEEAVILTYFPVVH 64
              ||:: ||:  | :|||  |:|||:  |:|          ::|:    :|    :::  |:
Db          8 KCIKYLLFGFNFIFWLAGIAVLAIGLWLR--------FDSQTKSIFEQETNHSSFYTGVY 59

Qy         65 PVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVW--TYEQELMVP 122
               ::|     :::|| || || |: :  :|  :|| ||||| :|:|  ||  |:: |::
Db         60 -ILIGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAAAVWGYTHKDEVIKE 118

Qy        123 VQ--WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              :|  : |       :: |   |:   |              |||:       :|    |  |
Db        119 LQEFYKDTY---QKLRNKDEPQRETL----KAIHMALNCCGI---AGGVEQFISDICPKK 168

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
                :  |          :   |    |    | :          ::  :|| | |  |  ||
Db        169 QVLESF-------QVKSCPDAIDEVFHSKFH----------IIGAVGIGIAVVMIFGMIF 211

Qy        241 TITLLWALYYDR 252
              :: |  |:  |
Db        212 SMILCCAIRRSR 223


RESULT 13
A36056
tumor-associated antigen CO-029 - human
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1990 #sequence_revision 09-Aug-1996 #text_change 20-Apr-2000
C;Accession: A36056
R;Szala, S.; Kasai, Y.; Steplewski, Z.; Rodeck, U.; Koprowski, H.; Linnenbach, A.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 6833-6837, 1990
A;Title: Molecular cloning of cDNA for the human tumor-associated antigen CO-029 and ide
A;Reference number: A36056; MUID:90370878; PMID:2395876
A;Accession: A36056
A;Molecule type: mRNA
A;Residues: 1-237 <SZA>
A;Cross-references: GB:M35252; NID:g180925; PIDN:AAA35709.1; PID:g180926
C;Genetics:
A;Gene: GDB:TM4SF3
A;Cross-references: GDB:9113496; OMIM:600769
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-33/Domain: transmembrane #status predicted <TM1>
F;34-52/Domain: extracellular #status predicted <EX1>
F;53-78/Domain: transmembrane #status predicted <TM2>
F;79-82/Domain: intracellular #status predicted <CY2>
F;83-107/Domain: transmembrane #status predicted <TM3>
F;108-205/Domain: extracellular #status predicted <EX2>
F;206-232/Domain: transmembrane #status predicted <TM4>
F;233-237/Domain: intracellular #status predicted <CY3>
F;37,118/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             12.4%;  Score 204;  DB 1;  Length 237;
  Best Local Similarity   25.5%;  Pred. No. 4.5e-11;
  Matches   64;  Conservative   53;  Mismatches   92;  Indels   42;  Gaps   12;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRV----EEAVILTYFPVVH 64
              |::  ::  | ||||  | :||:: |:|        :: :::     |:    :|  |
Db          7 CIKYSMFTFNFLFWLCGILILALAIWVR--------VSNDSQAIFGSEDVGSSSYVAV-- 56
```

```
Qy          65 PVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVW--TYEQELMVP 122
               ::|||   ::|:| || || :| :  :|  :|  ||:|  :::| |:   ::
Db          57 DILIAVGAIIMILGFLGCCGAIKESRCMLLLFFIGLLLILLLQVATGILGAVFKSK---- 112

Qy         123 VQWSDMVTLKARMTNYGL-----PRYRWLTHAWNFFQREFKCCGVVY-FTDWLEMTEMDW 176
                 || :  :    | |          :    || ||||||:|    ||
Db         113 ---SDRIVNETLYENTKLLSATGESEKQFQEAIIVFQEEFKCCGLVNGAADW--GNNFQH 167

Qy         177 PPDSC-CVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIG--VT 233
               |: | |: :   |     ::   :|:| |     ||::     ::  :||| |  |
Db         168 YPELCACLDKQRPCQSYNGKQ---VYKETC----ISFIKDFLAKNLIIVIGISFGLAVI 219

Qy         234 QILAMILTITL 244
               :|| :: :: |
Db         220 EILGLVFSMVL 230
```

```
RESULT 14
A35649
cell surface protein TAPA-1 - human
N;Alternate names: target of antiproliferative antibody (TAPA) 1
C;Species: Homo sapiens (man)
C;Date: 28-Sep-1990 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: A35649
R;Oren, R.; Takahashi, S.; Doss, C.; Levy, R.; Levy, S.
Mol. Cell. Biol. 10, 4007-4015, 1990
A;Title: TAPA-1, the target of an antiproliferative antibody, defines a new family of tr
A;Reference number: A35649; MUID:90318365; PMID:1695320
A;Accession: A35649
A;Molecule type: mRNA
A;Residues: 1-236 <ORE>
A;Cross-references: GB:M33680; NID:g338677; PIDN:AAA36663.1; PID:g338678
C;Genetics:
A;Gene: GDB:TAPA1
A;Cross-references: GDB:135038; OMIM:186845
A;Map position: 11p15.5-11p15.5
C;Superfamily: CD9 antigen
C;Keywords: transmembrane protein
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-57/Domain: extracellular #status predicted <EX1>
F;58-84/Domain: transmembrane #status predicted <TM2>
F;85-88/Domain: intracellular #status predicted <CY2>
F;89-113/Domain: transmembrane #status predicted <TM3>
F;114-203/Domain: extracellular #status predicted <EX2>
F;204-230/Domain: transmembrane #status predicted <TM4>
F;231-236/Domain: intracellular #status predicted <CY3>

  Query Match             12.1%;  Score 199;  DB 1;  Length 236;
  Best Local Similarity   24.2%;  Pred. No. 1.3e-10;
  Matches   63;  Conservative   44;  Mismatches  103;  Indels   50;  Gaps    8;

Qy           1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMR--DYLNNVLTLTAETRVEEAVILT 58
               |  |    ||:: ||:  | :|||    :| |: |:|       |:| |       ::    |
Db           1 MGVEGCTKCIKYLLFVFNFVFWLAGGVILGVALWLRHDPQTTNLLYLELG---DKPAPNT 57

Qy          59 YFPVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVW----- 113
               ::  :: ::|||   :: || ||  | :: :  ||  :|  |:::|  |:| |:|
Db          58 FYVGIY-ILIAVGAVMMFVGFLGCYGAIQESQCLLGTFFTCLVILFACEVAAGIWGFVNK 116

Qy         114 ---------TYEQELMVPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVY 164
                      |:| |    |    |    || :                 |      |||
Db         117 DQIAKDVKQFYDQALQQAVVDDDANNAKAVVKT--------------FHETLDCCGSST 161

Qy         165 FTDWLEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLR 224
               |    :|     : |          :   :|:|::| | :|:     |  :| ::
Db         162 LT---ALTTSVLKNNLC----------PSGSNIISNLFKEDCHQKIDDLFSG--KLYLIG 206

Qy         225 FLGISIGVTQILAMILTITL 244
                 | : |  |  |||:: |
Db         207 IAAIVVAVIMIFEMILSMVL 226
```

```
RESULT 15
A46472
cell surface protein TAPA-1 - mouse
N;Alternate names: target of antiproliferative antibody (TAPA) 1
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: A46472
R;Andria, M.L.; Hsieh, C.L.; Oren, R.; Francke, U.; Levy, S.
J. Immunol. 147, 1030-1036, 1991
A;Title: Genomic organization and chromosomal localization of the TAPA-1 gene.
A;Reference number: A46472; MUID:91318144; PMID:1650385
A;Accession: A46472
A;Molecule type: DNA
A;Residues: 1-236 <AND>
A;Cross-references: GB:S45012; NID:g1679982; PIDN:AAB19417.1; PID:g233253
A;Experimental source: B-cell lymphoma line 38C13
A;Note: sequence extracted from NCBI backbone (NCBIN:44957, NCBIN:44966, NCBIN:45001, NC
C;Superfamily: CD9 antigen
C;Keywords: transmembrane protein
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-57/Domain: extracellular #status predicted <EX1>
F;58-84/Domain: transmembrane #status predicted <TM2>
F;85-88/Domain: intracellular #status predicted <CY2>
F;89-113/Domain: transmembrane #status predicted <TM3>
F;114-203/Domain: extracellular #status predicted <EX2>
F;204-230/Domain: transmembrane #status predicted <TM4>
F;231-236/Domain: intracellular #status predicted <CY3>

  Query Match             11.8%;  Score 193;  DB 1;  Length 236;
  Best Local Similarity   24.8%;  Pred. No. 4.5e-10;
  Matches   64;  Conservative   38;  Mismatches  110;  Indels   46;  Gaps    7;

Qy           1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
               |  |    ||:: ||:  | :|||    :| |: |:|       |  |   : |    |
Db           1 MGVEGCTKCIKYLLFVFNFVFWLAGGVILGVALWLRHDPQTTSLLYLELGNKPAPNTFYV 60

Qy          61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVW------- 113
                :   ::|||   :: || ||  | :: :  ||  :|  |:::|  |:|.|:|
Db          61 GIY--ILIAVGAVMMFVGFLGCYGAIQESQCLLGTFFTCLVILFACEVAAGIWGFVNKDQ 118

Qy         114 -------TYEQELMVPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFT 166
                      |:| |    |    |    || :                 |     |||    |
Db         119 IAKDVKQFYDQALQQAVMDDDANNAKAVVKT--------------FHETLNCCGSNALT 163

Qy         167 DWLEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFL 226
               |  | :    :: |          :    |: | |: | :|:     |  :| ::
Db         164 T-LTTTIL---RNTLC----------PSGGNILTPLLQQDCHQKIDELFSG--KLYLIGIA 208

Qy         227 GISIGVTQILAMILTITL 244
                | : |  |  |||:: |
Db         209 AIVVAVIMIFEMILSMVL 226


Search completed: May 13, 2004, 16:08:16
Job time : 15.5752 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:01:35 ; Search time 39.4071 Seconds
(without alignments)
2442.024 Million cell updates/sec

Title: US-09-830-328C-2
Perfect score: 1642
Sequence: 1 MAREDSVKCLRCLLYALNLL.....IFEHTSMANSFNTHFEMEEL 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1636	99.6	305	4	Q8N5Y0	Q8n5y0 homo sapien
2	1615	98.4	305	11	Q8BKT6	Q8bkt6 mus musculu
3	1611	98.1	305	11	Q8BZU1	Q8bzu1 mus musculu
4	1111.5	67.7	301	13	Q7T2G0	Q7t2g0 brachydanio
5	287	17.5	253	11	Q921J7	Q921j7 mus musculu
6	280	17.1	253	4	Q86U54	Q86u54 homo sapien
7	274.5	16.7	239	11	Q8BJU2	Q8bju2 mus musculu
8	257.5	15.7	238	13	Q7SY95	Q7sy95 xenopus lae
9	252	15.3	253	11	Q9D1D1	Q9d1d1 mus musculu
10	240.5	14.6	248	13	Q7ZWZ1	Q7zwz1 xenopus lae
11	238.5	14.5	267	4	Q7Z2D4	Q7z2d4 homo sapien
12	237	14.4	227	13	Q7ZUH9	Q7zuh9 brachydanio
13	232.5	14.2	249	11	Q8BT06	Q8bt06 mus musculu
14	225	13.7	232	5	Q9XVI4	Q9xvi4 caenorhabdi
15	224	13.6	215	4	Q8N6Z9	Q8n6z9 homo sapien
16	217.5	13.2	228	13	Q8AV92	Q8av92 petromyzon
17	216.5	13.2	224	13	Q9IBC9	Q9ibc9 gallus gall
18	214.5	13.1	226	6	Q8MJ48	Q8mj48 sus scrofa
19	203	12.4	242	4	Q7Z5N2	Q7z5n2 homo sapien
20	202	12.3	236	6	Q7YRE9	Q7yre9 tupaia bela
21	202	12.3	249	13	Q7ZXL9	Q7zxl9 xenopus lae
22	199	12.1	222	13	Q8AV91	Q8av91 petromyzon
23	196	11.9	227	13	Q7SYR5	Q7syr5 xenopus lae
24	196	11.9	236	11	Q91V78	Q91v78 mus musculu
25	194.5	11.8	236	13	Q7ZTR5	Q7ztr5 xenopus lae
26	193.5	11.8	283	5	Q8MS10	Q8ms10 drosophila
27	191	11.6	244	4	Q7Z3Z6	Q7z3z6 homo sapien
28	191	11.6	244	6	Q7YQL0	Q7yql0 pan troglod
29	190	11.6	239	5	Q9NB10	Q9nb10 manduca sex
30	190	11.6	244	6	Q7YQK9	Q7yqk9 pongo pygma
31	189.5	11.5	283	11	Q8R3S2	Q8r3s2 mus musculu
32	188.5	11.5	248	5	Q9VLH1	Q9vlh1 drosophila
33	187.5	11.4	268	5	Q9V3X2	Q9v3x2 drosophila
34	186.5	11.4	265	13	Q802B9	Q802b9 xenopus lae
35	186	11.3	235	11	Q8R3G9	Q8r3g9 mus musculu
36	185.5	11.3	283	4	Q86UF1	Q86uf1 homo sapien
37	185	11.3	251	13	Q7SXT2	Q7sxt2 brachydanio
38	184	11.2	235	11	O55158	O55158 rattus norv
39	184	11.2	236	13	Q9DDS7	Q9dds7 brachydanio
40	182.5	11.1	282	5	Q19983	Q19983 caenorhabdi
41	182	11.1	245	11	Q8BPU2	Q8bpu2 mus musculu
42	181	11.0	253	11	Q80XR4	Q80xr4 mus musculu
43	180	11.0	204	11	Q8BTH3	Q8bth3 mus musculu
44	180	11.0	240	11	Q99J59	Q99j59 mus musculu
45	178.5	10.9	267	5	Q9V3E5	Q9v3e5 drosophila

ALIGNMENTS

RESULT 1
Q8N5Y0
ID Q8N5Y0 PRELIMINARY; PRT; 305 AA.
AC Q8N5Y0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transmembrane 4 superfamily member tetraspan NET-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC031265; AAH31265.1; -.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
SQ SEQUENCE 305 AA; 35356 MW; EC57D5E13A8E92DC CRC64;

Query Match 99.6%; Score 1636; DB 4; Length 305;
Best Local Similarity 99.7%; Pred. No. 3e-152;
Matches 304; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVISTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
```

```
Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 2
Q8BKT6
ID   Q8BKT6      PRELIMINARY;      PRT;   305 AA.
AC   Q8BKT6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Tetraspan NET-2 homolog.
GN   AI426782.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Body;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK050737; BAC34399.1; -.
DR   MGD; MGI:1889818; AI426782.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
SQ   SEQUENCE   305 AA;  35407 MW;  1C5C36D37F002F06 CRC64;

  Query Match           98.4%;  Score 1615;  DB 11;  Length 305;
  Best Local Similarity   98.0%;  Pred. No. 3.4e-150;
  Matches  299;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||:|
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGTLLVIFCVELACGVWTYEQEVM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNYFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||:||||| |||||| ||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMLSLKNDTSQHLSCHSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 3
Q8BZU1
ID   Q8BZU1      PRELIMINARY;      PRT;   305 AA.
AC   Q8BZU1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Tetraspan NET-2 homolog.
GN   AI426782.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Colon;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK033554; BAC28354.1; -.
DR   MGD; MGI:1889818; AI426782.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
SQ   SEQUENCE   305 AA;  35408 MW;  B8F15565A709E2B0 CRC64;

  Query Match           98.1%;  Score 1611;  DB 11;  Length 305;
  Best Local Similarity   97.7%;  Pred. No. 8.5e-150;
  Matches  298;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAREDSVECLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||:|
Db         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGTLLVIFCVELACGVWTYEQEVM 120

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNYFQREFKCCGVVYFTDWLEMTEMDWPPDS 180

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240

Qy        241 TITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHF 300
              ||||||||||||||||||:||||| |||||| ||||||||||||||||||||||||||||
Db        241 TITLLWALYYDRREPGTDQMLSLKNDTSQHLSCHSVELLKPSLSRIFEHTSMANSFNTHF 300

Qy        301 EMEEL 305
              |||||
Db        301 EMEEL 305


RESULT 4
Q7T2G0
ID   Q7T2G0      PRELIMINARY;      PRT;   301 AA.
AC   Q7T2G0;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
```

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RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054563; AAH54563.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   301 AA;  34093 MW;  C4CDA310F298C200 CRC64;

  Query Match             67.7%;  Score 1111.5;  DB 13;  Length 301;
  Best Local Similarity   66.9%;  Pred. No. 8.7e-101;
  Matches  208;  Conservative   40;  Mismatches   46;  Indels   17;  Gaps    4;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              |||||||||||||||||| |||||:: || |||::|| |||||||||:||:||| : ||
Db          1 MAREDSVKCLRCLLYALNFLFWLMALCVLGVSAYLRDQLNNVLTLTADTRLEEAAVRTYS 60

Qy         61 PVVHPVVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||||||:|||||||||| |:|||||:| |||||:||||||:|||||||| |||||:: :
Db         61 PVVHPVVIAVCCFLIIVAMVGYCGTLKCNLLLLSWYFGSLMVIFCVELASGVWTYDEPM- 119

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDS 180
                || |||::||:|| ::|| ||:|||||||  | | |||||:|||||||||||:|||||
Db        120 --VQRSDMISLKSRMPHFGLQRYQWLTHAWNALQTELKCCGVIYFTDWLEMTEMEWPPDS 177

Qy        181 CCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMIL 240
              ||  ::|||::|||  |||||||||||| |:|||:|||||||||||||:|||| ||||| |
Db        178 CCSNQYPGCARQAHYNDLSDLYQEGCGPKIYSFIRGTKQLQVLRFLGVSIGVAQILAMTL 237

Qy        241 TITLLWALYYDRREP---GTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMAN--- 294
              |:|||||||| : |     | ::          |   |: : || | |      : ||
Db        238 TVTLLWALYYDHKPPEPASADALI--------HTHSPTEDPLKVSHSHPRASEAWANTPA 289

Qy        295 SFNTHFEMEEL 305
              : :| ||||:|
Db        290 NGHTQFEMEQL 300


RESULT 5
Q921J7
ID   Q921J7      PRELIMINARY;      PRT;   253 AA.
AC   Q921J7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Similar to CD151 antigen.
GN   CD151.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012236; AAH12236.1; -.
DR   MGD; MGI:1096360; Cd151.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
SQ   SEQUENCE   253 AA;  28241 MW;  A4BEFB049253C311 CRC64;

  Query Match             17.5%;  Score 287;  DB 11;  Length 253;
  Best Local Similarity   29.5%;  Pred. No. 5.8e-20;
  Matches   75;  Conservative   48;  Mismatches   97;  Indels   34;  Gaps    9;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| | :        ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASS--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWS 126
                 ::: |:|| | | |    ||  ||  ||:|| :|:  |:  : | |:|   :: :
Db         66 VAGVVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYVYYQQLNTELKEN 125

Qy        127 DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW---------- 176
              |:  |   |   :  :| |  |:|| |||      ||     : :|
Db        126 LKDTMVKRYHQSG---HEGVTSAVDKLQQEFHCCGSNNSQDW---QDSEWIHSGEADSRV 179

Qy        177 PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQ 234
              |||||     || |: |    |::|  : ||  |: :|::  : |:|:  :|| |   |
Db        180 VPDSCCKTMVAGCGKRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIACVQ 234

Qy        235 ILAMILTITLLWAL 248
              :  || |  |  :|
Db        235 VFGMIFTCCLYRSL 248


RESULT 6
Q86U54
ID   Q86U54      PRELIMINARY;      PRT;   253 AA.
AC   Q86U54;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD151 antigen.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT007397; AAP36061.1; -.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
SQ   SEQUENCE   253 AA;  28295 MW;  0C8FE4CF2C3C286D CRC64;

  Query Match             17.1%;  Score 280;  DB 4;  Length 253;
  Best Local Similarity   29.8%;  Pred. No. 2.8e-19;
  Matches   76;  Conservative   46;  Mismatches   97;  Indels   36;  Gaps   10;

Qy          9 CLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMI 68
              ||: ||:  |  |||  ::|:||  |     :: ::| |          ||    : :::
Db         15 CLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASG--------TYLATAY-ILV 65

Qy         69 AVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWS 126
                 ::: |:|| | | |    ||  ||  ||:|| :|:  |:  : | |:|   ::
Db         66 VAGTVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYAYYQQLNTELK-- 123
```

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Qy        127 DMVTLKARMT-NYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDW--------- 176
Db        124 --ENLKDTMTKRYHQPGHEAVTSAVDQLQQEFHCCGSNNSQDW---RDSEWIRSQEAGGR 178

Qy        177 -PPDSCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIGVT 233
Db        179 VVPDSCCKTVVALCGQRDH---ASNIYKVEGGCITKLETFIQ--EHLRVIGAVGIGIACV 233

Qy        234 QILAMILTITLLWAL 248
Db        234 QVFGMIFTCCLYRSL 248
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RESULT 7
Q8BJU2
ID Q8BJU2 PRELIMINARY; PRT; 239 AA.
AC Q8BJU2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tetraspan NET-5 homolog (Hypothetical protein).
GN 9430079M16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK079139; BAC37559.1; -.
DR EMBL; BC052503; AAH52503.1; -.
DR MGD; MGI:1924558; 9430079M16Rik.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Hypothetical protein.

```
SQ   SEQUENCE   239 AA;  26737 MW;  B3DC47ADA1D877DD CRC64;

  Query Match             16.7%;  Score 274.5;  DB 11;  Length 239;
  Best Local Similarity   29.2%;  Pred. No. 9.1e-19;
  Matches   74;  Conservative   40;  Mismatches  110;  Indels   29;  Gaps    7;

Qy          9 CLRCLLYAL---NLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHP 65
Db          5 CLCCLKYTMFLFNLIFWLCGCGLLGVGIWLSVSQGNFATFSPS----------FPSLSA 53

Qy         66 --VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPV 123
Db         54 ANLVIAIGTIVMVTGFLGCLGAIKENKCLLLSFFIVLLIILLAELILIILFF--VYMDKV 111

Qy        124 QWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCV 183
Db        112 NENAKQDLKEGLLLYNTENNVGLKNAWNIIQAEMRCCGVTDYTDWYPVLGENTVPDRCCM 171

Qy        184 REFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTIT 243
Db        172 ENSQGCGRNS----TTPLWRTGCYEKVKLWFDDNK--HVLGTVGMCILIMQILGMAFSMT 225

Qy        244 LLWALY-----YD 251
Db        226 LFQHIHRTGKKYD 238
```

RESULT 8
Q7SY95
ID Q7SY95 PRELIMINARY; PRT; 238 AA.
AC Q7SY95;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Klein S., Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054957; AAH54957.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   238 AA;  25757 MW;  032D4D875A2A4F7D CRC64;

  Query Match             15.7%;  Score 257.5;  DB 13;  Length 238;
  Best Local Similarity   25.0%;  Pred. No. 4.2e-17;
  Matches   62;  Conservative   58;  Mismatches  105;  Indels   23;  Gaps    7;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              ||  |  :||:: |::  | :||:  |:::|:  :::  ||: | :          :::
Db          1 MAVEGGMKCVKFLMFFFNFVFWVCGIALIAIGIYVQIQLNHTLIMKNAASSGAPIVV--- 57

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
                 ::: |  |||     | || :| |  ::  :   |::|| ||:|  :  |  :
Db         58 -----IVVGVVIFLI--AFFGCCGALKENYCMVTTFAVVLVLIFLVEIAAAIAAYVYKDK 110

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLE---MTEMDWP 177
               :  : | : |  |: |   :  :| : :  |:||||||    ||| :       |
Db        111 LRTAFED--SFKNGMSKYNTTKD--ITESIDLLQKEFKCCGAFNATDWKQYPPFNGTDAV 166

Qy        178 PDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILA 237
              |||||     || |   :  : : :||  :  :::  | : ::  : : | : :||
Db        167 PDSCCKTIIAGCGK----DPSATINTDGCATGIDQWVK--KNIGIVAGVALGIALFEILG 220

Qy        238 MILTITLL 245
               :|    |:
Db        221 IIFACCLM 228


RESULT 9
Q9D1D1
ID   Q9D1D1      PRELIMINARY;      PRT;   253 AA.
AC   Q9D1D1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   1110014F12Rik protein (Weakly similar to platelet-endothelial
DE   tetraspan antigen 3).
GN   1110014F12RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Colon, Eye, and Skin;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK003691; BAB22942.1; -.
DR   EMBL; AK028808; BAC26129.1; -.
DR   EMBL; AK053788; BAC35523.1; -.
DR   EMBL; AK090022; BAC41051.1; -.
DR   MGD; MGI:1915748; 1110014F12Rik.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
SQ   SEQUENCE   253 AA;  28072 MW;  8A820157A945C60A CRC64;

  Query Match             15.3%;  Score 252;  DB 11;  Length 253;
  Best Local Similarity   29.6%;  Pred. No. 1.6e-16;
  Matches   73;  Conservative   40;  Mismatches  104;  Indels   30;  Gaps    8;

Qy         10 LRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMIA 69
              |: ||:  |  ||:   :|:||  |          ||  ::     :  : |     ::|
Db         16 LKYLLFIFNFFFWVGGAAVMAVGIW---------TLVEKSGYLSILASSTFAASAYILIF 66

Qy         70 VCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQELMVPVQWSD 127
              |   ::  | ||:   ::      |: ||  ||||| |||  ||    | | |   ::|
Db         67 VGGLVMTTGFLGFGAIIREQKSCLSTYFCLLLVIFLVELVAGVLAHVYYQRLSDELKWH- 125

Qy        128 MVTLKARMT-NYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM-------DWPPD 179
                | : :| :|| ||   :| : :  |::|||||     ||     :          ||
Db        126 ---LNSTLTEHYGQPRAAEITASVDRLQQDFKCCGSNSSADWQHSAYILSQEALGRQVPD 182

Qy        180 SCCVREFPGCSKQAHQEDLSDLY--QEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILA 237
              |||       | ::||    |::|  : ||  |:  |:      | ::  :|| :   ||
Db        183 SCCKTVVARCGQRAHP---SNIYKVEGGCMAKLEQFV--ADHLLLMGAVGIGVACLQICG 237

Qy        238 MILTITL 244
              |:||  |
Db        238 MVLTCCL 244


RESULT 10
Q7ZWZ1
ID   Q7ZWZ1      PRELIMINARY;      PRT;   248 AA.
AC   Q7ZWZ1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to CD63 antigen (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046575; AAH46575.1; -.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   248 AA;  27115 MW;  DC1801E256C7E6B6 CRC64;

  Query Match             14.6%;  Score 240.5;  DB 13;  Length 248;
  Best Local Similarity   24.2%;  Pred. No. 2.1e-15;
  Matches   61;  Conservative   55;  Mismatches  105;  Indels   31;  Gaps    7;
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Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              || |  :||:: |::  | :||:  |:::|:  :::  ||: | :   |     :
Db          9 MAVEGGMKCVKFLMFFFNFVFWVCGIALIAIGIYVQIQLNHTLIMKNATSSGTPI----- 63

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGV--WTYEQE 118
                 :| |   : ::   | || :| |  ::  :   |::|| ||:|  :  : |: :
Db         64 -----AIIVVGLVIFLIAFFGCCGALKENYCMVTTFAVVLVLIFLVEIAAAIAAYVYKDK 118

Qy        119 LMVPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWP- 177
              |    : |     |  |: |     : :  : :  |:|||||    ||| :
Db        119 LRTAFBES----FKDGMSRYN--NTKEMADSIDLLQKEFKCCGAFNSTDWKQYAPFVGTT 172

Qy        178 --PDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQI 235
                |||||     || |     : :  :||   :  :::        : :|| ||
Db        173 NVPDSCCKNITAGCGKAPFPP--NSINTDGCANGIDQWVK--------KNIGIVAGVALG 222

Qy        236 LAMILTITLLWA 247
                :|:  |: :::|
Db        223 IALFETLGIIFA 234


RESULT 11
Q7Z2D4
ID   Q7Z2D4      PRELIMINARY;      PRT;   267 AA.
AC   Q7Z2D4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Kangai 1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC000726; AAH00726.1; -.
DR   EMBL; BC001821; AAH01821.1; -.
SQ   SEQUENCE   267 AA;  29611 MW;  FC3786A4521CABDE CRC64;

  Query Match             14.5%;  Score 238.5;  DB 4;  Length 267;
  Best Local Similarity   27.0%;  Pred. No. 3.5e-15;
  Matches   71;  Conservative   51;  Mismatches  100;  Indels   41;  Gaps   10;

Qy          7 VKCLRCLLYALNLLFWLMSISVLAVSAWM----RDYLNNVLTLTAETRVEEAVILTYFPV 62
              :|  :  |:  ||:|:::  :|     |:      ::: : | ::  |:          |
Db          6 IKVTKYFLFLFNLIFFILGAVILGFGVWILADKSSFISVLQTSSSSLRMG-----AY--- 57

Qy         63 VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVP 122
                 | |  |    :::| ||  | |     ||  ||  ||:|   ::  |   |     :
Db         58 ---VFIGVGAVTMLMGFLGCIGAVNEVRCLLGLYFAFLLLILIAQVTAGALFYFNMGKLK 114

Qy        123 VQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTE-MDWP---- 177
               :  :||   |  :|   |   |  ||:: | : |||| | | :| :  | |: |
Db        115 QEMGGIVTELIR--DYNSSREDSLQDAWDYVQAQVKCCGWVSFYNWTDNAELMNRPEVTY 172

Qy        178 PDSCCVR--------------EFPGCSKQA--HQEDLSDLYQEGCGKKMYSFLRGTKQLQ 221
              | || |:              | ||   |:  | ||   :|||| :|: ::|:  : |
Db        173 PCSCEVKGEEDNSLSVRKGFCEAPGNRTQSGNHPEDW-PVYQEGCMEKVQAWLQ--ENLG 229

Qy        222 VLRFLGISIGVTQILAMILTITL 244
              ::  :|: : : ::| |:|:| |
Db        230 IILGVGVGVAIVELLGMVLSICL 252


RESULT 12
Q7ZUH9
ID   Q7ZUH9      PRELIMINARY;      PRT;   227 AA.
AC   Q7ZUH9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Body;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC049036; AAH49036.1; -.
DR   InterPro; IPR008952; Tetraspanin.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00421; TM4_1; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   227 AA;  24362 MW;  A48AEBAA2B74B100 CRC64;

  Query Match             14.4%;  Score 237;  DB 13;  Length 227;
  Best Local Similarity   28.9%;  Pred. No. 4.1e-15;
  Matches   73;  Conservative   42;  Mismatches  100;  Indels   38;  Gaps   10;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILT-- 58
              ||     ::|:: ||:  | :|||    ||||  |:|       |||     : | ||
Db          1 MAAGGGLQCIKYLLFIFNFIFWLAGTGVLAVGLWLRFDAKTKEFFTAEN--GQTVFLTGV 58

Qy         59 YFPVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVW--TYE 116
              |       ::|     :::|| || || :| :  :|  :|  |||||  :| |:|  : :
Db         59 Y------ILIVAGAVMMVVGFLGCCGAIKESACMLGLFFMFLLVIFAAEVAAGIWGLSNK 112

Qy        117 QELMVPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVV-YFTDWLEMTEMD 175
               :::  ||     |:|    :   |    || | :|     :|||     :| : :|
Db        113 DKIVSDVQQFYTQTVKNYKESPDGPLKETLT-AIHF---SLQCCGPTGLASDGVSVT--- 165

Qy        176 WPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQI 235
                        | |   || |:::   ||   :       :| |:  :|| |||  :
Db        166 ------------CPK---QEGLANVITTGCSSVIQDMF--NSRLHVIGGVGIGIGVIMV 207

Qy        236 LAMILTITLLWAL 248
                || :: |  |:
Db        208 FGMIFSMLLCCAI 220
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RESULT 13
Q8BT06
ID   Q8BT06      PRELIMINARY;      PRT;   249 AA.
AC   Q8BT06;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cd63 antigen.
GN   CD63.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Body;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK028220; BAC25821.1; -.
DR   MGD; MGI:99529; Cd63.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005386; F:carrier activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000264; Serum_albumin.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
DR   PROSITE; PS00212; ALBUMIN; 1.
DR   PROSITE; PS00421; TM4_1; 1.
SQ   SEQUENCE   249 AA;  26784 MW;  E2716D4FC9482443 CRC64;

  Query Match           14.2%;  Score 232.5;  DB 11;  Length 249;
  Best Local Similarity   27.9%;  Pred. No. 1.3e-14;
  Matches   69;  Conservative   48;  Mismatches  109;  Indels   21;  Gaps    8;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              || |  :||:: ||| | | |   :: ::|:   ::  |   :|         |    :
Db         12 MAVEGGMKCVKFLLYVLLLAFCACAVGLIAIGVAVQVVLKQAIT-------HETTAGSLL 64

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||    |:|||  || :|  :| ||  | |  |:  :   | :|  ||:|  :  |
Db         65 PV---VIIAVGAFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAVAIAGYVFRDQ 121

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM--DWPP 178
              |  :::   : : :| || |   :  |   :  |:|  |||   :|||  :  |  |  |
Db        122 VKSEFNK--SFQQQMQNY-LKDNKTAT-ILDKLQKENNCCGASNYTDWENIPGMAKDRVP 177

Qy        179 DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAM 238
              ||||:    ||      :   | :: :|| : :  :||  | : ::    : |   ::| :
Db        178 DSCCININTVGCGNDFKE---STIHTQGCVETIAIWLR--KNILLVAAAALGIAFVEVLGI 232

Qy        239 ILTITLL 245
              | :  |:
Db        233 IFSCCLV 239


RESULT 14
Q9XVI4
ID   Q9XVI4      PRELIMINARY;      PRT;   232 AA.
AC   Q9XVI4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T23D8.2 protein.
GN   T23D8.2.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wild A.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z81128; CAB03397.2; -.
DR   PIR; T25161; T25161.
DR   WormPep; T23D8.2; CE26006.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
SQ   SEQUENCE   232 AA;  25206 MW;  1073713036131492 CRC64;

  Query Match           13.7%;  Score 225;  DB 5;  Length 232;
  Best Local Similarity   25.8%;  Pred. No. 6.3e-14;
  Matches   64;  Conservative   50;  Mismatches   96;  Indels   38;  Gaps    9;

Qy          4 EDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVV 63
              |  |  :: ||:  ||: |:  :|:: | : ::   :||| :  : |:   ::|
Db          3 EGGVTIVKYLLFLANLVLWVGGLSLIIVGSILQLKFDNVLDILGDERLATPILL------ 56

Qy         64 HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPV 123
                ::|   | |:  | || || :: |  |  :  | ::   :|  :  |
Db         57 --LVIGSLCTLL--GFLGCCGAIRENYCLTVSFAVLLALLITCEIAAVIIGYALH----- 107

Qy        124 QWSDMVTLK-ARMTNYGLPRY---RWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPD 179
                 |    |          |: ||   | :  ||:   : |:||||   :|||  | :   ||
Db        108 ---DSFRLGIGNQLQTGMVRYHESRGVESAWDKTHQLFECCGVTNSSDWLTFTTI---PD 161

Qy        180 SCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMI 239
              |||: |  ||:::      : |:: ||       :   :|  ||:   :  |:  :|| |
Db        162 SCCIEEIEGCAREN-----APLFEPGC-------IHSVEQ-WVLKNGAMVGGICAVLAAI 208

Qy        240 LTITLLWA 247
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Db        209 QLVGVCFA 216


RESULT 15
Q8N6Z9
ID   Q8N6Z9      PRELIMINARY;      PRT;   215 AA.
AC   Q8N6Z9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Lysosome-associated membrane protein-3 variant.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Ancans J., Suzuki I., Thody A.J.;
RT   "Melanocyte variant of lysosome-associated membrane protein-3 (LAMP3;
RT   also CD63 and melanoma associated antigen ME419) mRNA.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF508304; AAM34259.1; -.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005386; F:carrier activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000264; Serum_albumin.
DR   InterPro; IPR000301; Transmem_4.
DR   Pfam; PF00335; transmembrane4; 1.
DR   PRINTS; PR00259; TMFOUR.
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DR   PROSITE; PS00212; ALBUMIN; 1.
DR   PROSITE; PS00421; TM4_1; 1.
SQ   SEQUENCE   215 AA;  23430 MW;  C4469E42BCC8C4F7 CRC64;

  Query Match             13.6%;  Score 224;  DB 4;  Length 215;
  Best Local Similarity   26.7%;  Pred. No. 7.3e-14;
  Matches   66;  Conservative   43;  Mismatches   94;  Indels   44;  Gaps    7;

Qy          1 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYF 60
              || |  :||:: ||| | | |                                |   :
Db          1 MAVEGGMKCVKFLLYVLLLAFC----------------------------GATPGSLL 30

Qy         61 PVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELM 120
              ||    |:|||  || :|  :| || | |  |:  :    | :|  ||:|  :  |
Db         31 PV---VIIAVGVFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDK 87

Qy        121 VPVQWSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEM--DWPP 178
              |  ::::    : :| ||  |:        :  | :|||||   :||| ::  |  :  |
Db         88 VMSEFNN--NFRQQMENY--PKNNHTASILDRMQADFKCCGAANYTDWEKIPSMSKNRVP 143

Qy        179 DSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAM 238
              ||||:    ||    :::    :::||| :|:  :||  | : |:    : |   ::| :
Db        144 DSCCINVTVGCGINFNEK---AIHKEGCVEKIGGWLR--KNVLVVAAAALGIAFVEVLGI 198

Qy        239 ILTITLL 245
              :    |:
Db        199 VFACCLV 205


Search completed: May 13, 2004, 16:07:37
Job time : 40.4071 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 08:41:32 ; Search time 1151.36 Seconds
(without alignments)
10909.949 Million cell updates/sec

Title: US-09-830-328C-4
Perfect score: 2768
Sequence: 1 tcgacgccaccatttaaag.....tagagagtaaaaaaaaaaaa 2768

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2393.8	86.5	2397	10	US-09-946-374-272	Sequence 272, App
2	2393.8	86.5	2397	12	US-10-015-395A-272	Sequence 272, App
3	2393.8	86.5	2397	13	US-10-206-915-323	Sequence 323, App
4	2393.8	86.5	2397	13	US-10-199-670-323	Sequence 323, App
5	2393.8	86.5	2397	13	US-10-201-858-323	Sequence 323, App
6	2393.8	86.5	2397	13	US-10-205-890-323	Sequence 323, App
7	2393.8	86.5	2397	13	US-10-208-024-323	Sequence 323, App
8	2393.8	86.5	2397	13	US-10-201-853-323	Sequence 323, App
9	2393.8	86.5	2397	13	US-10-063-745-107	Sequence 107, App
10	2393.8	86.5	2397	13	US-10-063-512-107	Sequence 107, App
11	2393.8	86.5	2397	13	US-10-063-513-107	Sequence 107, App
12	2393.8	86.5	2397	13	US-10-063-549-107	Sequence 107, App
13	2393.8	86.5	2397	13	US-10-063-569-107	Sequence 107, App
14	2393.8	86.5	2397	13	US-10-063-551-107	Sequence 107, App
15	2393.8	86.5	2397	13	US-10-174-581-323	Sequence 323, App
16	2393.8	86.5	2397	13	US-10-176-483-323	Sequence 323, App
17	2393.8	86.5	2397	13	US-10-176-749-323	Sequence 323, App
18	2393.8	86.5	2397	13	US-10-176-914-323	Sequence 323, App
19	2393.8	86.5	2397	13	US-10-176-915-323	Sequence 323, App
20	2393.8	86.5	2397	13	US-10-006-485A-272	Sequence 272, App
21	2393.8	86.5	2397	13	US-10-013-907A-272	Sequence 272, App
22	2393.8	86.5	2397	13	US-10-015-499A-272	Sequence 272, App
23	2393.8	86.5	2397	13	US-10-063-555-107	Sequence 107, App
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25	2393.8	86.5	2397	13	US-10-063-594-107	Sequence 107, App
26	2393.8	86.5	2397	13	US-10-063-553-107	Sequence 107, App
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28	2393.8	86.5	2397	13	US-10-176-484-323	Sequence 323, App
29	2393.8	86.5	2397	13	US-10-180-550-323	Sequence 323, App
30	2393.8	86.5	2397	13	US-10-183-014-323	Sequence 323, App
31	2393.8	86.5	2397	13	US-10-187-738-323	Sequence 323, App
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33	2393.8	86.5	2397	13	US-10-187-883-323	Sequence 323, App
34	2393.8	86.5	2397	13	US-10-194-363-323	Sequence 323, App
35	2393.8	86.5	2397	13	US-10-194-460-323	Sequence 323, App
36	2393.8	86.5	2397	13	US-10-194-463-323	Sequence 323, App
37	2393.8	86.5	2397	13	US-10-194-484-323	Sequence 323, App
38	2393.8	86.5	2397	13	US-10-195-884-323	Sequence 323, App
39	2393.8	86.5	2397	13	US-10-195-896-323	Sequence 323, App
40	2393.8	86.5	2397	13	US-10-196-744-323	Sequence 323, App
41	2393.8	86.5	2397	13	US-10-196-755-323	Sequence 323, App
42	2393.8	86.5	2397	13	US-10-196-757-323	Sequence 323, App
43	2393.8	86.5	2397	13	US-10-197-704-323	Sequence 323, App
44	2393.8	86.5	2397	13	US-10-197-710-323	Sequence 323, App
45	2393.8	86.5	2397	13	US-10-198-758-323	Sequence 323, App

ALIGNMENTS

RESULT 1
US-09-946-374-272
; Sequence 272, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
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; PRIOR APPLICATION NUMBER: 60/105807

Query Match 86.5%; Score 2393.8; DB 10; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
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Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

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Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
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Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
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Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
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Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
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Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
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Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 2
US-10-015-395A-272
; Sequence 272, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 272
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-395A-272

Query Match 86.5%; Score 2393.8; DB 12; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080
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Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 3
US-10-206-915-323
; Sequence 323, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 323
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-206-915-323

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60
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Qy       422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
Db        61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy       482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
Db       121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA-180

Qy       542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
Db       181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy       602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
Db       241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy       662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
Db       301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy       722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
Db       361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy       782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db       421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy       842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db       481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy       902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
Db       541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy       962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
Db       601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy      1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db       661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy      1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db       721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy      1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db       781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy      1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
Db       841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy      1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db       901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy      1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
Db       961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy      1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
Db      1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy      1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
Db      1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy      1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
Db      1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy      1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
Db      1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy      1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
Db      1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy      1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
Db      1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy      1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
Db      1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy      1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
Db      1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy      1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
Db      1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy      1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
Db      1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy      1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db      1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy      2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db      1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy      2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db      1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy      2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db      1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy      2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db      1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy      2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db      1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy      2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
Db      1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy      2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
Db      2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy      2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
Db      2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy      2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
Db      2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy      2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
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Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397


RESULT 4
US-10-199-670-323
; Sequence 323, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C401
;  CURRENT APPLICATION NUMBER: US/10/199,670
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 323
;   LENGTH: 2397
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-199-670-323

  Query Match             86.5%;  Score 2393.8;  DB 13;  Length 2397;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2395;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy      -1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
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Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681

Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741

Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801

Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861

Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921

Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981

Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041

Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101

Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161

Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221

Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281

Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341

Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401

Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461

Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521

Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581

Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641

Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701

Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758

Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 5
US-10-201-858-323
; Sequence 323, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 323
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-858-323

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421

Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481

Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541

Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
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Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240
Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300
Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360
Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420
Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480
Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540
Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600
Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660
Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720
Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780
Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840
Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900
Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960
Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020
Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080
Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140
Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200
Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260
Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
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Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320
Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380
Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440
Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500
Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560
Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620
Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680
Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740
Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800
Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860
Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920
Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980
Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040
Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100
Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160
Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220
Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280
Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340
Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 6
US-10-205-890-323
; Sequence 323, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C519
;  CURRENT APPLICATION NUMBER: US/10/205,890
;  CURRENT FILING DATE:  2002-07-26
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 323
;   LENGTH: 2397
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-205-890-323

  Query Match             86.5%;  Score 2393.8;  DB 13;  Length 2397;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2395;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380
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Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
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Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
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Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
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Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
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Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
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RESULT 7
US-10-208-024-323
; Sequence 323, Application US/10208024

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; Publication No. US20040048335A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C538
;  CURRENT APPLICATION NUMBER: US/10/208,024
;  CURRENT FILING DATE:  2002-07-29
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 323
;   LENGTH: 2397
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-208-024-323
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Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360
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Qy       722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
Db       361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy       782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db       421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy       842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db       481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy       902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
Db       541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy       962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
Db       601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy      1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db       661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy      1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db       721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy      1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db       781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy      1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
Db       841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy      1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db       901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy      1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
Db       961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy      1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
Db      1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy      1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
Db      1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy      1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
Db      1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy      1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
Db      1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy      1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
Db      1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy      1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
Db      1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy      1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
Db      1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy      1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
Db      1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy      1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
Db      1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy      1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
Db      1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy      1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db      1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy      2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db      1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy      2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db      1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy      2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db      1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy      2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db      1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy      2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db      1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy      2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
Db      1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy      2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
Db      2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy      2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
Db      2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy      2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
Db      2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy      2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
Db      2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy      2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
Db      2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy      2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
Db      2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 8
US-10-201-853-323
; Sequence 323, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc

; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 323
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-853-323

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
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Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 9
US-10-063-745-107
; Sequence 107, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,745
;  CURRENT FILING DATE:  2002-05-09
;      Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 107
;   LENGTH: 2397
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-063-745-107

  Query Match             86.5%;  Score 2393.8;  DB 13;  Length 2397;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2395;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840
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Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 10
US-10-063-512-107
; Sequence 107, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 107
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-107

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
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Db      121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180
Qy      542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
Db      181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240
Qy      602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
Db      241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300
Qy      662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
Db      301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360
Qy      722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
Db      361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420
Qy      782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db      421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480
Qy      842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db      481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540
Qy      902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
Db      541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600
Qy      962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
Db      601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660
Qy     1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db      661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720
Qy     1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db      721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780
Qy     1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db      781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840
Qy     1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
Db      841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900
Qy     1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db      901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960
Qy     1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
Db      961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020
Qy     1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
Db     1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080
Qy     1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
Db     1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140
Qy     1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
Db     1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200
Qy     1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
Db     1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260
Qy     1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
Db     1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320
Qy     1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
Db     1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380
Qy     1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
Db     1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440
Qy     1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
Db     1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500
Qy     1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
Db     1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560
Qy     1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
Db     1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620
Qy     1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db     1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680
Qy     2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db     1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740
Qy     2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db     1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800
Qy     2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db     1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860
Qy     2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db     1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920
Qy     2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db     1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980
Qy     2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
Db     1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040
Qy     2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
Db     2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100
Qy     2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
Db     2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160
Qy     2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
Db     2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220
Qy     2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
Db     2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280
Qy     2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
Db     2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340
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Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397


RESULT 11
US-10-063-513-107
; Sequence 107, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,513
;  CURRENT FILING DATE:  2002-05-01
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 107
;   LENGTH: 2397
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-063-513-107

  Query Match             86.5%;  Score 2393.8;  DB 13;  Length 2397;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2395;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy        2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy        2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy        2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy        2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy        2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy        2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy        2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy        2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy        2522 CCAGAAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2161 CCAGAAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy        2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy        2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy        2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 12
US-10-063-549-107
; Sequence 107, Application US/10063549
; Publication No. US20030027986A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,549
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 107
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-549-107

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  Query Match             86.5%;  Score 2393.8;  DB 13;  Length 2397;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2395;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy         422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy         482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy         542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy         602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy         662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy         722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy         782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy         842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy         902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy         962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy        1022 TTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 TTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy        1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy        1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy        1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy        1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960
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Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 13
US-10-063-569-107
; Sequence 107, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 107
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-107

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
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Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300
Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360
Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420
Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480
Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540
Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600
Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660
Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720
Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780
Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840
Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900
Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960
Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020
Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080
Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140
Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200
Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260
Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320
Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380
Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440
Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500
Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560
Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620
Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680
Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740
Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800
Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860
Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920
Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980
Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040
Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100
Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160
Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220
Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280
Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340
Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 14
US-10-063-551-107

; Sequence 107, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 107
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-107

Query Match 86.5%; Score 2393.8; DB 13; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
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Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 15
US-10-174-581-323
; Sequence 323, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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  Query Match             86.5%;  Score 2393.8;  DB 13;  Length 2397;
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  Matches 2395;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
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Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
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Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
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Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
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Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
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Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
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Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
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Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660
Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720
Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780
Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840
Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900
Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960
Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020
Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080
Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140
Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200
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Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320
Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380
Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440
Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500
Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560
Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620
Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680
Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740
Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800
Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860
Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920
Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980
Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040
Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
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Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160
Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220
Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280
Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340
Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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Search completed: May 17, 2004, 20:29:31
Job time : 1155.36 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 01:41:21 ; Search time 1058.17 Seconds
(without alignments)
11112.549 Million cell updates/sec

Title: US-09-830-328C-4
Perfect score: 2768
Sequence: 1 tcgacgccaccatttaaag.....tagagagtaaaaaaaaaaa 2768

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2768	100.0	2768	3	AAA27100	Aaa27100 cDNA enco
2	2393.8	86.5	2397	3	AAA37098	Aaa37098 Human PRO
3	2393.8	86.5	2397	4	AAF54395	Aaf54395 DNA encod
4	2393.8	86.5	2397	4	AAS46086	Aas46086 Human DNA
5	2393.8	86.5	2397	4	AAF92111	Aaf92111 Human PRO
6	2393.8	86.5	2397	6	ABS74431	Abs74431 Human cDN
7	2393.8	86.5	2397	7	ABX78689	Abx78689 Human PRO
8	2393.8	86.5	2397	7	ACA75661	Aca75661 Novel hum
9	2393.8	86.5	2397	7	ACA71141	Aca71141 Human sec
10	2393.8	86.5	2397	7	ACC87669	Acc87669 Human sec
11	2393.8	86.5	2397	7	ACC87055	Acc87055 Human sec
12	2393.8	86.5	2397	7	ACD04228	Acd04228 Human sec
13	2393.8	86.5	2397	7	ACA69559	Aca69559 cDNA enco
14	2393.8	86.5	2397	7	ACA90404	Aca90404 Novel hum
15	2393.8	86.5	2397	7	ACC89511	Acc89511 Human sec
16	2393.8	86.5	2397	7	ACA98302	Aca98302 Novel hum
17	2393.8	86.5	2397	7	ACA93944	Aca93944 Human sec
18	2393.8	86.5	2397	7	ACD15337	Acd15337 Human sec
19	2393.8	86.5	2397	7	ACD08924	Acd08924 Human sec
20	2393.8	86.5	2397	7	ACC96844	Acc96844 Human sec
21	2393.8	86.5	2397	7	ACF15565	Acf15565 Human sec
22	2393.8	86.5	2397	7	ACA72932	Aca72932 Human PRO
23	2393.8	86.5	2397	7	ACD03104	Acd03104 Novel hum
24	2393.8	86.5	2397	7	ACD01919	Acd01919 Novel hum
25	2393.8	86.5	2397	7	ACA92111	Aca92111 Novel hum
26	2393.8	86.5	2397	7	ACA89536	Aca89536 cDNA enco
27	2393.8	86.5	2397	7	ACA73546	Aca73546 Human sec
28	2393.8	86.5	2397	7	ACA05861	Aca05861 Human sec
29	2393.8	86.5	2397	7	ACA66695	Aca66695 cDNA enco
30	2393.8	86.5	2397	7	ACA91217	Aca91217 Novel hum
31	2393.8	86.5	2397	7	ACD81594	Acd81594 Human cDN
32	2393.8	86.5	2397	7	ACF20270	Acf20270 Human sec
33	2393.8	86.5	2397	7	ACF19656	Acf19656 Human sec
34	2393.8	86.5	2397	7	ACD21944	Acd21944 Human sec
35	2393.8	86.5	2397	7	ACF13109	Acf13109 Human sec
36	2393.8	86.5	2397	7	ACD25212	Acd25212 Human sec
37	2393.8	86.5	2397	7	ACF00261	Acf00261 Human sec
38	2393.8	86.5	2397	7	ACA60416	Aca60416 Novel hum
39	2393.8	86.5	2397	7	ACA72318	Aca72318 Novel hum
40	2393.8	86.5	2397	7	ACD04842	Acd04842 Novel hum
41	2393.8	86.5	2397	7	ACD18303	Acd18303 Human sec
42	2393.8	86.5	2397	7	ACD08310	Acd08310 Human sec
43	2393.8	86.5	2397	7	ACA88744	Aca88744 Novel hum
44	2393.8	86.5	2397	7	ACA70186	Aca70186 Human sec
45	2393.8	86.5	2397	7	ACD12408	Acd12408 Novel hum

ALIGNMENTS

RESULT 1
AAA27100
ID AAA27100 standard; cDNA; 2768 BP.
XX
AC AAA27100;
XX
DT 28-JUL-2000 (first entry)
XX
DE cDNA encoding human TM4P-2.
XX
KW Human; transmembrane 4 protein; TM4P; tetraspan; cancer;
KW developmental disorder; cell proliferation disorder;
KW immunological disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 569. .1486
FT /*tag= a
FT /product= "TM4P-2"
XX
PN WO200026243-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025499.
XX
PR 29-OCT-1998; 98US-0172249P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Argentine CC, Corley NC, Gorgone GA, Guegler KJ;
PI Baughn MR;
XX
DR WPI; 2000-376122/32.
DR P-PSDB; AAY94420.
XX
PT Human transmembrane 4 proteins (TM4P) useful for diagnosis, treatment and
PT prevention of disorders associated with expression of TM4P such as
PT developmental disorders.
XX
PS Claim 9; Fig 2; 86pp; English.
XX
CC Human transmembrane 4 protein (TM4P) is involved in development,
CC inflammation and cell proliferation. The protein acts through signal
CC transduction, control of cell adhesion and regulation of cell growth. A

CC pharmaceutical composition of TM4P could be used to treat a condition
CC associated with disrupted expression of TM4P, such as immunological,
CC developmental and cell proliferation disorders. In addition antibodies
CC which specifically bind TM4P may be used for the diagnosis of disorders
CC characterised by expression of TM4P. The present sequence is the cDNA
CC encoding human TM4P-2 from Incyte Clone 2674553. This clone was derived
CC from kidney tissue cDNA library KIDNNOT19
XX
SQ Sequence 2768 BP; 789 A; 530 C; 607 G; 842 T; 0 U; 0 Other;

Query Match 100.0%; Score 2768; DB 3; Length 2768;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCGACGCCACCATTTTAAAGGGATTTACTGCACGGACTTCTCCCAAGTTCCTAGGCATTA 60
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Db          1 TCGACGCCACCATTTTAAAGGGATTTACTGCACGGACTTCTCCCAAGTTCCTAGGCATTA 60

Qy         61 TCTTCTGGACCCTATCCTGCAGAGGTGAAGCGTCCCTTTGGGGACTCTCGCTGGGTGAGA 120
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Db        121 GGGACAAGAAACACCCACTAGGACCCAACCCCGGCAGCCAGCGGCTCGAGCATGCGCTGA 180

Qy        181 GAGTTTGTGCAGCTGGCCCTGGCTGCCGCCGCTGCCTCGTCCGGACTCGGAGAGGACTTG 240
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Qy        301 ACTTTTTTTTTTTTTTTTCTTTTTCCCAGGAGGCGGCGACGGCGGCGGCGGGGGGGAGAGG 360
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Qy        361 AAGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGT 420
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Qy        421 TCCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCA 480
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Qy        541 ATGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCG 600
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Qy        601 CTGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGT 660
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Qy        661 TTCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGT 720
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Qy        781 CTGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTT 840
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Db        781 CTGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTT 840

Qy        841 GCTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGG 900
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Qy        901 CGTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTT 960
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Qy        961 GAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAA 1020
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Qy       1021 TTTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAAT 1080
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Qy       1081 GACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAA 1140
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Qy       1201 TTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGG 1260
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Qy       1321 TAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCT 1380
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Qy       1381 GTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATC 1440
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Qy       1501 GAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTT 1560
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Qy       1741 ACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAA 1800
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Qy       1981 GTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCA 2040
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Db       2761 AAAAAAAA 2768
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ID AAA37098 standard; cDNA; 2397 BP.
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AC AAA37098;
XX
DT 08-AUG-2000 (first entry)
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DE Human PRO1568 (UNQ774) cDNA sequence SEQ ID NO:272.
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KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.

XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
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XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2000-237871/20.
DR   P-PSDB; AAY99416.
XX
PT   New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT   PRO polypeptides, useful for screening of potential peptide or small
PT   molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS   Claim 2; Fig 153; 773pp; English.
XX
CC   AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC   receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC   transmembrane and receptor PRO proteins can be used for screening of
CC   potential peptide or small molecule inhibitors of the relevant
CC   receptor/ligand interactions. The polypeptides and nucleotide sequences
CC   encoding then have various industrial applications, including uses as
CC   pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC   primers and hybridisation probes used in the isolation of the PRO
CC   polypeptides from the present invention
XX
SQ   Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;

  Query Match            86.5%;  Score 2393.8;  DB 3;  Length 2397;
  Best Local Similarity   99.9%;  Pred. No. 0;
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Qy       362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
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Qy       482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
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Qy       542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
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Db       181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy       602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy       662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy       722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy       782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy       842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy       902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy       962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy      1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy      1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy      1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy      1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy      1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381

Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441

Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501

Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561

Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621

Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681

Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741

Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801

Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861

Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921

Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981

Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041

Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101

Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161

Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221

Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281

Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341

Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401

Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461

Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521

Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581

Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641

Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701

Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758

Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
```

RESULT 3
AAF54395
ID AAF54395 standard; DNA; 2397 BP.
XX
AC AAF54395;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA encoding protein of the invention #75.
XX
KW Secreted; transmembrane; gene therapy; ss.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US004342.
XX
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Claim 2; Fig 149; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.

CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;

Query Match 86.5%; Score 2393.8; DB 4; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
Db        541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
Db       1141 AAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1200

Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
Db       1321 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1380

Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db       1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ATAAGAAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2160

Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
```

RESULT 4
AAS46086
ID AAS46086 standard; cDNA; 2397 BP.
XX
AC AAS46086;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #162.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR P-PSDB; AAU29185.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
PS Claim 2; Fig 323; 774pp; English.
XX
CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;

  Query Match   86.5%; Score 2393.8; DB 4; Length 2397;
  Best Local Similarity 99.9%; Pred. No. 0;
  Matches 2395; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
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Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
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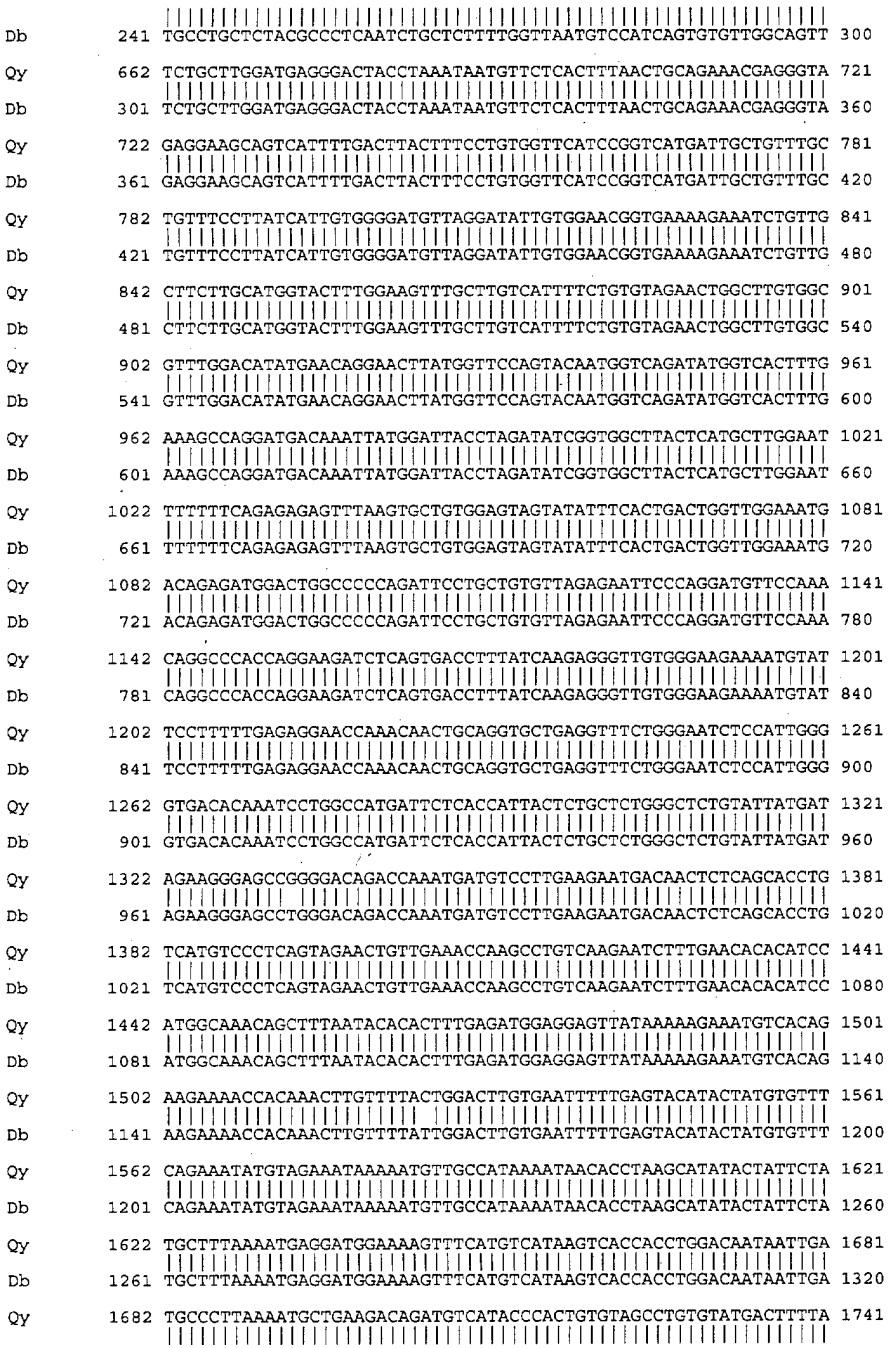

RESULT 5
AAF92111

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ID   AAF92111 standard; cDNA; 2397 BP.
XX
AC   AAF92111;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1568 cDNA.
XX
KW   Human; PRO protein; mapping; ss.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US023328.
XX
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   07-DEC-1999;   99US-0169495P.
PR   09-DEC-1999;   99US-0170262P.
PR   11-JAN-2000; 2000US-0175481P.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   03-MAR-2000; 2000US-0187202P.
PR   21-MAR-2000; 2000US-0191007P.
PR   30-MAR-2000; 2000WO-US008439.
PR   25-APR-2000; 2000US-0199397P.
PR   22-MAY-2000; 2000WO-US014042.
PR   05-JUN-2000; 2000US-0209832P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   P-PSDB; AAB87579.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT   biology, including use as hybridization probes, and in chromosome and
PT   gene mapping.
XX
PS   Claim 2; Fig 107; 278pp; English.
XX
CC   The present sequence is the coding sequence for a human PRO polypeptide
CC   (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC   antagonists or anti-PRO antibodies are useful for preparation of a
CC   medicament useful in the treatment of a condition which is responsive to
CC   the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC   protein may also be employed as molecular weight markers for protein
CC   electrophoresis. The PRO coding sequence has applications in molecular
CC   biology, including use as hybridisation probes, and in chromosome and
CC   gene mapping
XX
SQ   Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;

  Query Match             86.5%;  Score 2393.8;  DB 4;  Length 2397;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2395;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy        422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 240

Qy        602 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTT 300

Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 360

Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 420

Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
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Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
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Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
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Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
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Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
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Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
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Db        901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy       1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
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Db        961 AGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1020

Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
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Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
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Db       1201 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1260

Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
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Db       1261 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1320

Qy       1682 TGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTA 1741
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Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1620

Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
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Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
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Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
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Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
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Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
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Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
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Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
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Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
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Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
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Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
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Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 6
ABS74431
ID ABS74431 standard; cDNA; 2397 BP.
XX
AC ABS74431;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1568.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
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PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.

PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
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PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR P-PSDB; ABG95904.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 2; Fig 107; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 2397 BP; 713 A; 429 C; 491 G; 764 T; 0 U; 0 Other;

Query Match 86.5%; Score 2393.8; DB 6; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db         1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy       422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 120

Qy       482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
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Db       121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

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Query Match 86.5%; Score 2393.8; DB 7; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DT 07-JUL-2003 (first entry)
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KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
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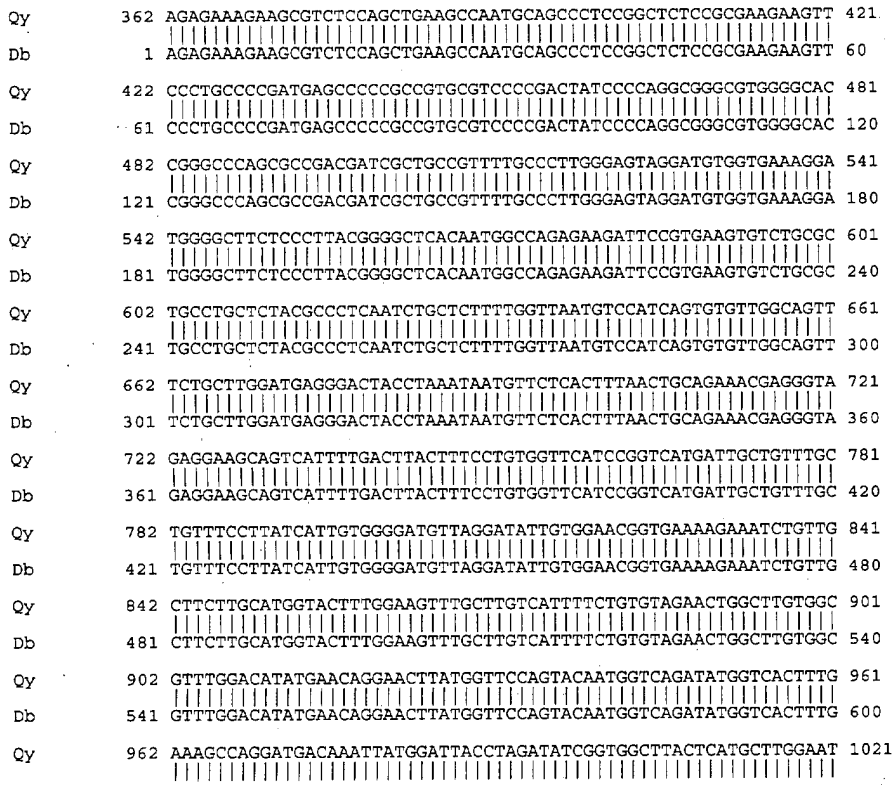

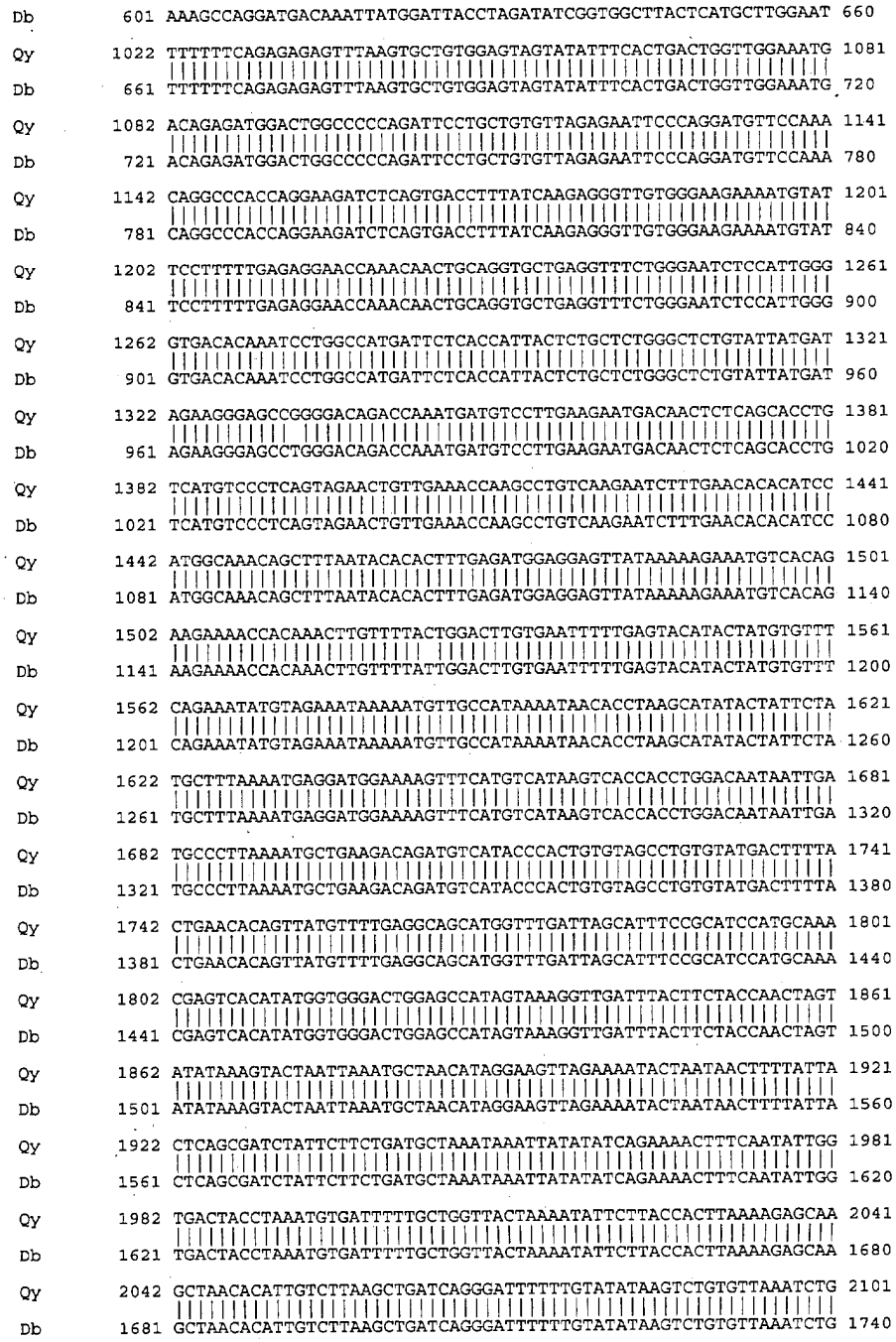

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DT 05-AUG-2003 (first entry)
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
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XX
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XX
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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Query Match 86.5%; Score 2393.8; DB 7; Length 2397;
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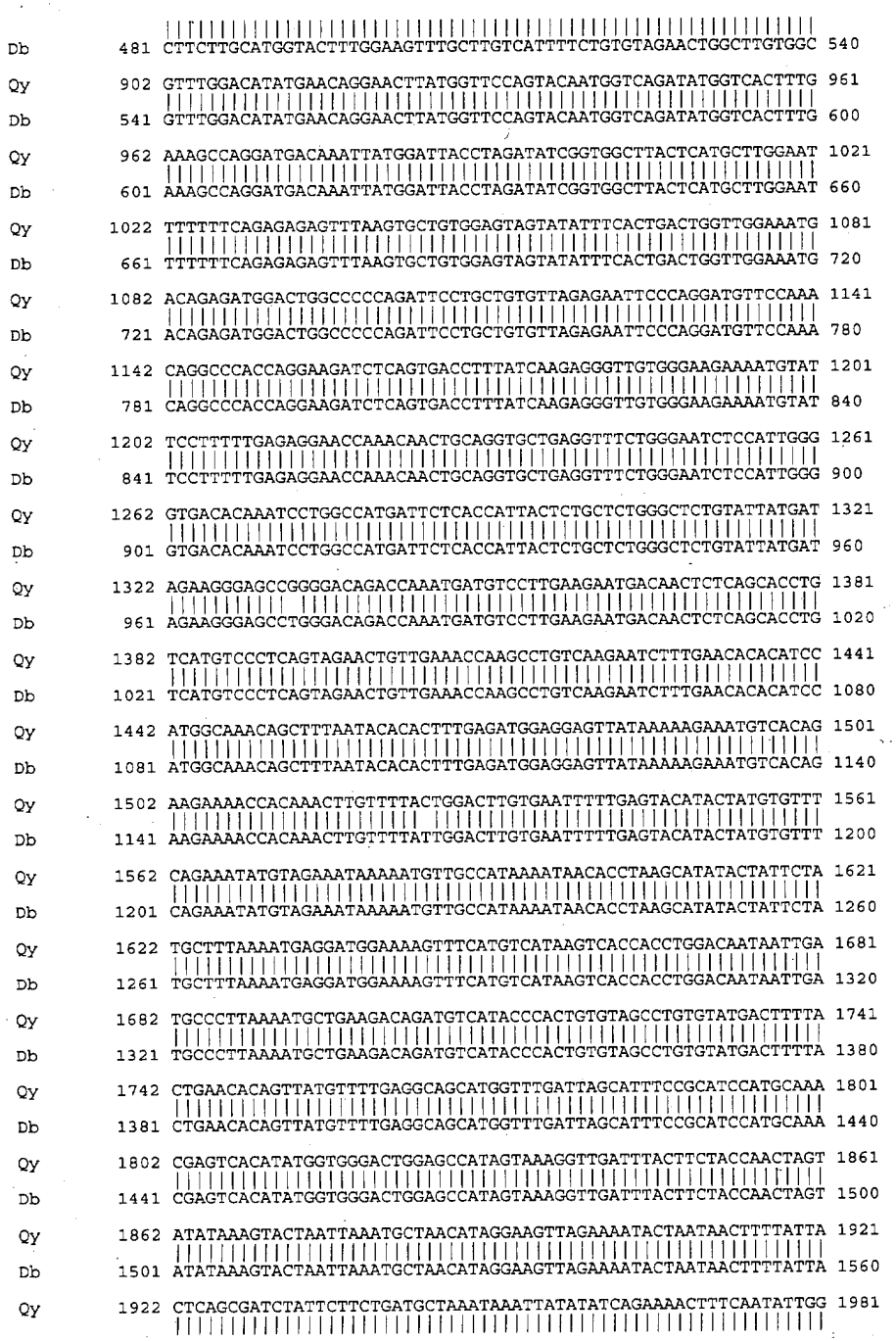

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Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 14
ACA90404
ID ACA90404 standard; cDNA; 2397 BP.
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AC ACA90404;
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DT 11-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1568 cDNA.
XX
KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
KW chondrocyte differentiation; tumour necrosis factor-alpha release; ss;
KW affinity purification; gene.
XX
OS Homo sapiens.

XX
PN US2003036147-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187741.
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Query Match 86.5%; Score 2393.8; DB 7; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db        1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

Qy      422 CCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCAC 481
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Qy      482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
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Qy      542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
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Qy       782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db       421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy       842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db       481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy       902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
Db       541 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 600

Qy       962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
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Qy      1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db       661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy      1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
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Qy      1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
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Db       841 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 900

Qy      1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
Db       901 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 960

Qy      1322 AGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTG 1381
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Qy      1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
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Qy      1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
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Qy      1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
Db      1621 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 1680

Qy      2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db      1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy      2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
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Qy      2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db      1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy      2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db      1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy      2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
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RESULT 15
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ID ACC89511 standard; cDNA; 2397 BP.
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AC ACC89511;
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DT 11-AUG-2003 (first entry)
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XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;

KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003027264-A1.
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PD 06-FEB-2003.
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PF 18-JUN-2002; 2002US-00174579.
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Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
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Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
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Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
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Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
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Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
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Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
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Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
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Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
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Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
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Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
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Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
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Search completed: May 17, 2004, 08:36:37
Job time : 1064.17 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 07:47:11 ; Search time 7165.47 Seconds
(without alignments)
11535.678 Million cell updates/sec

Title: US-09-830-328C-4
Perfect score: 2768
Sequence: 1 tcgacgccaccatttaaag.....tagagagtaaaaaaaaaaaa 2768

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
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14: gb_est5:*
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23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1202.2	43.4	2491	11	AK050737	AK050737 Mus muscu
2	1178	42.6	2325	11	AK033554	AK033554 Mus muscu
3	841.4	30.4	918	29	AY416016	AY416016 Homo sapi
4	815.4	29.5	1201	13	BX384369	BX384369 BX384369
c 5	775.6	28.0	846	12	BG210632	BG210632 RST30065
6	775.6	28.0	894	14	CD557440	CD557440 AGENCOURT
7	762.4	27.5	831	12	BG218523	BG218523 RST38146
8	758.6	27.4	926	10	BF338835	BF338835 602036272
9	731.6	26.4	783	14	CD656678	CD656678 AGENCOURT
10	708.6	25.6	918	29	AY416018	AY416018 Mus muscu
c 11	697	25.2	703	13	BU688134	BU688134 UI-CF-EC1
12	690.8	25.0	762	12	BG203659	BG203659 RST23047
13	682.8	24.7	700	13	BX487248	BX487248 DKFZp686P
14	662.8	23.9	918	29	AY416017	AY416017 Pan trogl
15	642.2	23.2	826	12	BG538289	BG538289 602566759
16	641.8	23.2	645	12	BG573872	BG573872 602593312
17	639.2	23.1	953	10	BF793959	BF793959 602254587
18	638	23.0	639	12	BM712366	BM712366 UI-E-DW1-
19	632.8	22.9	773	12	BG196478	BG196478 RST15700
20	629.4	22.7	683	12	BG260639	BG260639 602372203
21	628.4	22.7	810	12	BG189261	BG189261 RST8305 A
22	628	22.7	923	13	BX390738	BX390738 BX390738
23	623.8	22.5	773	13	BU612526	BU612526 UI-M-FR0-
24	616.4	22.3	633	9	AL709924	AL709924 DKFZp686N
25	612.2	22.1	933	13	BQ930962	BQ930962 AGENCOURT
26	606	21.9	617	14	CD679576	CD679576 hq13c06.y
27	601.2	21.7	627	10	BF971421	BF971421 602272941
28	601	21.7	602	12	BM723162	BM723162 UI-E-EO1-
29	597.2	21.6	649	12	BG570596	BG570596 602591281
30	588.8	21.3	725	10	BF029896	BF029896 601557058
c 31	587.6	21.2	760	12	BG211420	BG211420 RST30982
32	586.2	21.2	591	12	BI964728	BI964728 ie55g07.y
33	585	21.1	868	10	BF132023	BF132023 601821018
34	584	21.1	780	14	CD356773	CD356773 AGENCOURT
c 35	568.4	20.5	570	12	BI963141	BI963141 ie55g07.x
36	568.4	20.5	570	13	BX480472	BX480472 DKFZp686J
c 37	565	20.4	573	9	AI654147	AI654147 ty62d02.x
38	561.8	20.3	616	12	BG564912	BG564912 602589873
c 39	556.4	20.1	856	12	BG203576	BG203576 RST22960
c 40	550	19.9	550	9	AI810992	AI810992 tu10a10.x
41	548.4	19.8	557	12	BM697453	BM697453 UI-E-DX0-
42	545.6	19.7	808	12	BI851646	BI851646 603378869
43	545.4	19.7	764	13	BU278491	BU278491 603862459
44	523	18.9	883	12	BG921723	BG921723 602825551
45	514	18.6	514	12	BM760080	BM760080 K-EST0040

ALIGNMENTS

RESULT 1
AK050737
LOCUS AK050737 2491 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030012P12 product:TETRASPAN NET-2 homolog [Homo sapiens], full insert sequence.
ACCESSION AK050737
VERSION AK050737.1 GI:26341473
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

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REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2491)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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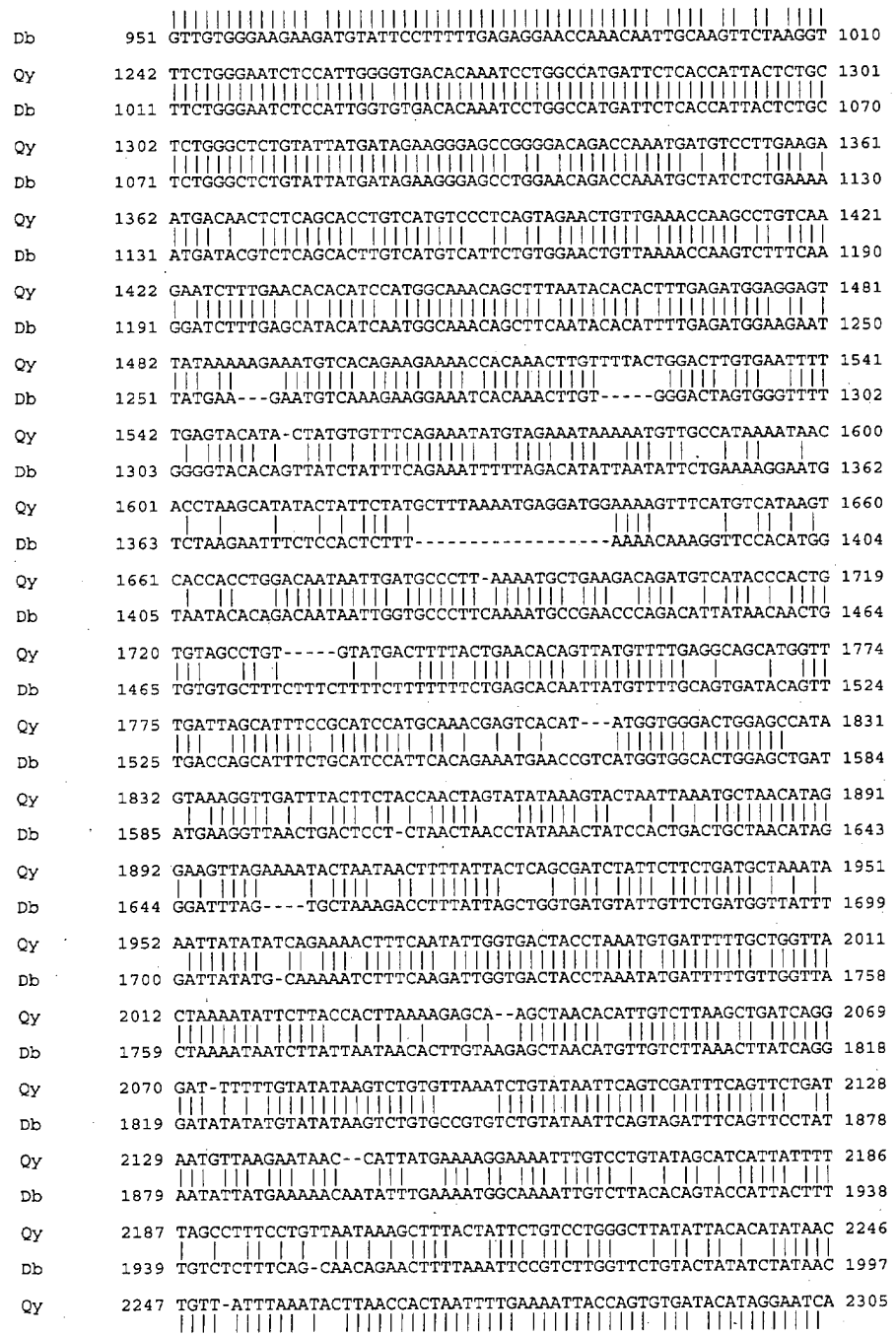

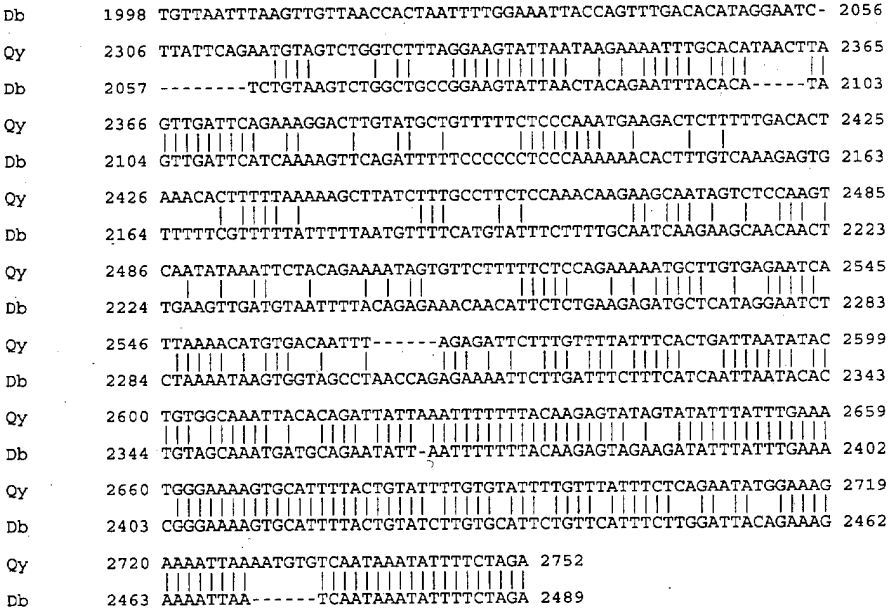

RESULT 2
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DEFINITION Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030619E17 product:TETRASPAN NET-2 homolog [Homo sapiens], full insert sequence.
ACCESSION AK033554
VERSION AK033554.1 GI:26329230
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

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  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2325)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
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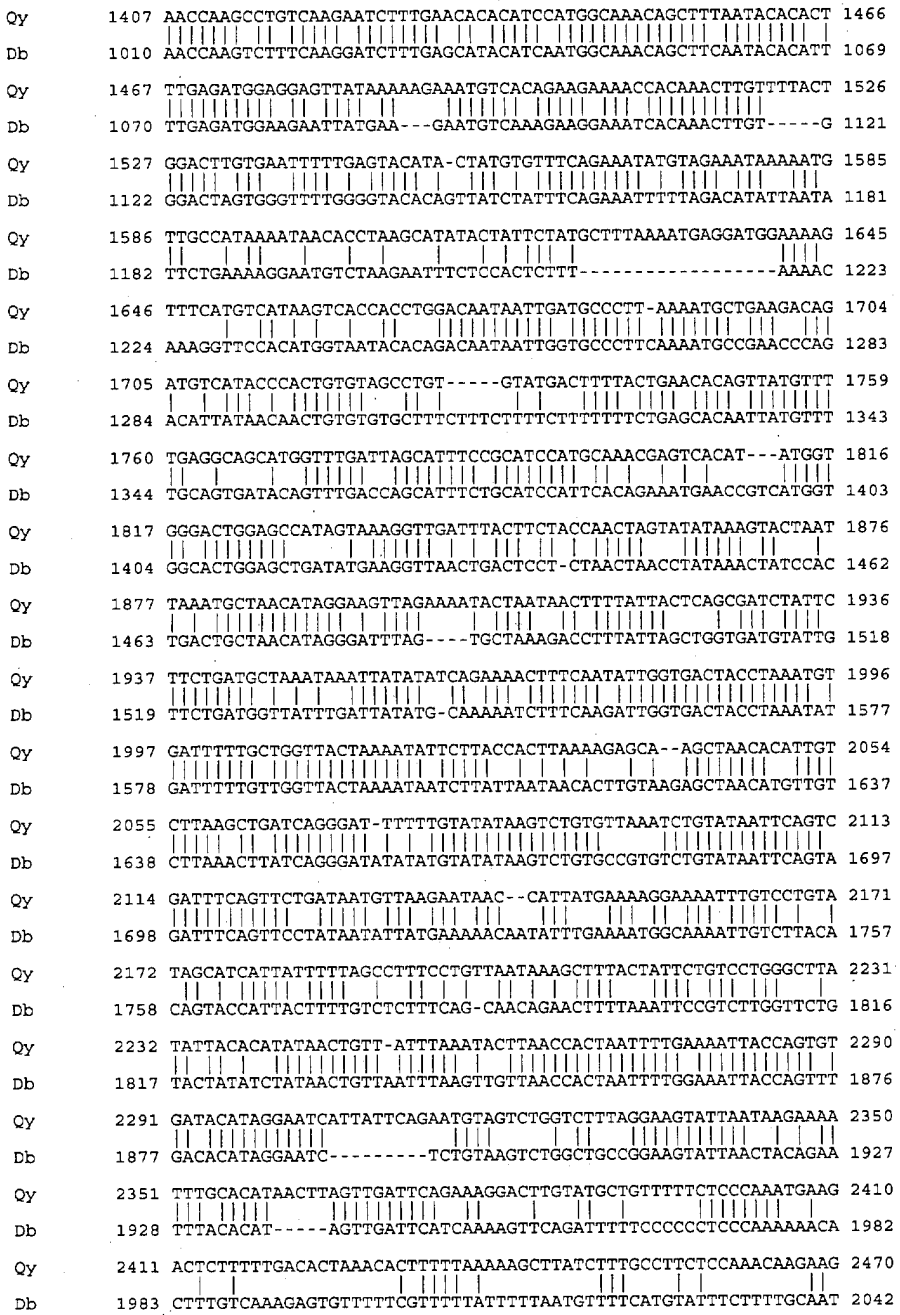

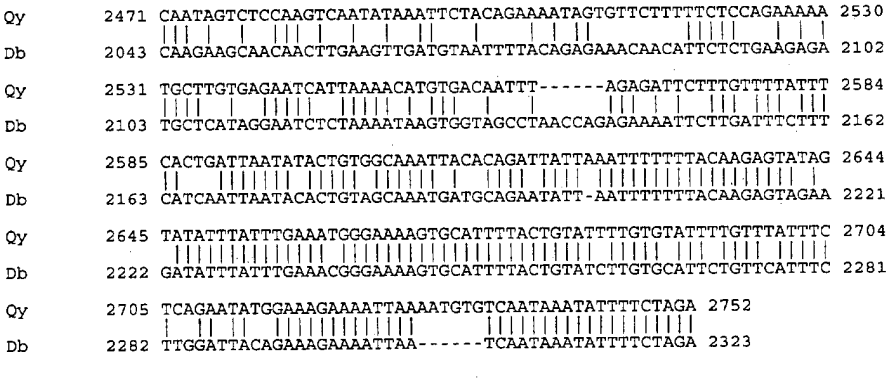

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VERSION AY416016.1 GI:39771976
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 918)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 918)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
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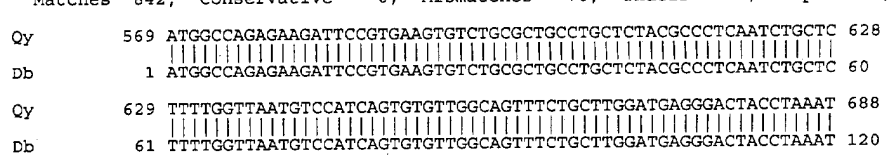
Matches 842; Conservative 0; Mismatches 76; Indels 0; Gaps 0;



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Qy        689 AATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTT 748
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Db        121 AATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTT 180

Qy        749 CCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTA 808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTA 240

Qy        809 GGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTG 868
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGNNNNNNNNNNNNNNN 300

Qy        869 CTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACTTATG 928
Db        301 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy        929 GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTA 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTA 420

Qy        989 CCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAGAGTTTAAGTGCTGT 1048
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Db        421 CCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAGAGTTTAAGTGCTGT 480

Qy       1049 GGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCC 1108
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Db        481 GGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCC 540

Qy       1109 TGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGAC 1168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGAC 600

Qy       1169 CTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTG 1228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTG 660

Qy       1229 CAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTC 1288
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Db        661 CAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTC 720

Qy       1289 ACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATG 1348
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Db        721 ACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATG 780

Qy       1349 ATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAA 1408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAA 840

Qy       1409 CCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTT 1468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTT 900

Qy       1469 GAGATGGAGGAGTTATAA 1486
              ||||||||||||||||||
Db        901 GAGATGGAGGAGTTATAA 918
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RESULT 4
BX384369
LOCUS       BX384369.                1201 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX384369 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK009YO01 5-PRIME, mRNA sequence.
ACCESSION   BX384369
VERSION     BX384369.1  GI:30455236
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D. .
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4017.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DK009AH01QP1&cluster=4017.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DK009AH01QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK009YO01"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

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  Query Match           29.5%;  Score 815.4;  DB 13;  Length 1201;
  Best Local Similarity  96.0%;  Pred. No. 1e-142;
  Matches  866;  Conservative   11;  Mismatches   18;  Indels    7;  Gaps    4;

Qy        369 GAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTGCC 428
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         65 GATGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTNCC 124

Qy        429 CCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCC 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCC 184

Qy        489 AGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCT 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCT 244

Qy        549 TCTCCCTTACGGGGCTCACAATGGCCAGAG-AAGATTCCGTGAAGTGTCTGCGCTGCCTG 607
              |||||||||||||||||||||||||||||: |||||||||| ||||||||||||||||||
Db        245 TCTCCCTTACGGGGCTCACAATGGCCAGARTAAGATTCCGTTAAGTGTCTGCGCTGCCTG 304

Qy        608 CTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCT 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCT 364

Qy        668 TGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAA 727
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Db        365 TGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAA 424

Qy        728 GCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTC 787
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        425 GCAGTCATTTTGACTTACTTTCCTGT--TTCATCCGGTCATGATTGCTGTTTGCTGTTTC 482

Qy        788 CTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTT 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTT 542

Qy        848 GCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGG 907
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Db        543 GCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGG 602

Qy        908 ACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCC 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 ACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCC 662

Qy        968 AGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTT 1027
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Db        663 AGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTT 722

Qy       1028 CAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAG 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAG 782

Qy       1088 ATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCC 1147
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Db        783 ATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCC 842

Qy       1148 CACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTT 1207
              |||||||||||||||||||||||||||||||||||||||||||||||||||      | : |||
Db        843 CACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCYTTTT 902

Qy       1208 TTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACA 1267
                ||   | | ||||:|||||||||| |::|:||:|||||||:|||:|:|| ||||  |:|
Db        903 GAGA---GGAACAAAMAACTGCAGG-GSYGRGGKTTCTGGGRATCYCMATGGGGGGAAMA 958

Qy       1268 CA 1269
                |
Db        959 AA 960


RESULT 5
BG210632/c
LOCUS       BG210632                846 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST30065 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG210632
VERSION     BG210632.1  GI:13732207
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 846)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 512.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
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                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match             28.0%;  Score 775.6;  DB 12;  Length 846;
  Best Local Similarity   97.7%;  Pred. No. 3.4e-135;
  Matches  818;  Conservative    0;  Mismatches   15;  Indels    4;  Gaps    3;

Qy       1782 CATTTCCGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTG 1841
              |||||||||||||| |||||||||||||||  |  |||  |||||||||||||| ||||

Db        840 CATTTCCGCATCCA-GCAAACGAGTCACATA--GGTGGAACGGAGCCATAGTAAA-GTTG 785

Qy       1842 ATTTACTTCTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAA 1901
              |||||||||| |||||||||||||||||||| | ||  |||| |||||| ||||||||
Db        784 ATTTACTTCTCCCAACTAGTATATAAAGTACTATTAAATGGCTACCATAGGCAGTTAGAA 725

Qy       1902 AATACTAATAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATAT 1961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 AATACTAATAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATAT 665

Qy       1962 CAGAAAACTTTCAATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATT 2021
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAGAAAACTNTCAATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATT 605

Qy       2022 CTTACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTAT 2081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CTTACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTAT 545

Qy       2082 ATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATA 2141
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Db        544 ATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATA 485

Qy       2142 ACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTA 2201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTA 425

Qy       2202 ATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTATTTAAATACT 2261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 ATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTATTTAAATACT 365

Qy       2262 TAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGT 2321
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Db        364 TAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGT 305

Qy       2322 CTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGA 2381
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Db        304 CTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGA 245

Qy       2382 CTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAA 2441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAA 185

Qy       2442 GCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACA 2501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCTTATCTTTGCCTTCTCCAAACAAGGAGCAATAGTCTCCAAGTCAATATAAATTCTACA 125

Qy       2502 GAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAA 2561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAA 65

Qy       2562 TTTAGAGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGAT 2618
              |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||
Db         64 TTTAGAGATTCTTTGTTTTATTTCACTGATTAATATACTATGGCAAATAACACAGAT 8


RESULT 6
CD557440
LOCUS       CD557440                894 bp    mRNA    linear   EST 11-JUN-2003
DEFINITION  AGENCOURT_14413568 NIH_MGC_180 Homo sapiens cDNA clone
            IMAGE:30387819 5', mRNA sequence.
ACCESSION   CD557440
VERSION     CD557440.1  GI:31583508
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
```

```
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM458  row: 1  column: 04
            High quality sequence stop: 610.
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                      /clone_lib="NIH_MGC_180"
                      /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: NotI;
                      Site_2: EcoRV (destroyed); Library is oligo-dT primed and
                      directionally cloned (EcoRV site is destroyed upon
                      cloning). Average insert size 1.68 kb. Library was
                      constructed by (Invitrogen). Note: this is a NIH_MGC
                      Library."
ORIGIN

  Query Match             28.0%;  Score 775.6;  DB 14;  Length 894;
  Best Local Similarity   97.1%;  Pred. No. 3.3e-135;
  Matches  799;  Conservative    0;  Mismatches   22;  Indels    2;  Gaps    1;

Qy        645 TCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAA 704
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Db          6 TCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAA 65

Qy        705 CTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGG 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGG 125

Qy        765 TCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGG 824
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Db        126 TCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGG 185

Qy        825 TGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTG 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 TGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTG 245

Qy        885 TAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGT 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGT 305

Qy        945 CAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGC 1004
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Db        306 CAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGC 365

Qy       1005 TTACTCATGCTTGGAATTTTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCA 1064
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Qy       1065 CTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAAT 1124
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Db        426 CTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAAT 485

Qy       1125 TCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTT 1184
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Qy       1185 GTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTC 1244
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Qy       1245 TGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCT 1304
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Db        606 TGGGAATCTCCATTGNGGTGACACANATCCTGGGCATGATTCTCACCATTACTCTGCTCT 665

Qy       1305 GGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATG 1364
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Db        666 GGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATG 725

Qy       1365 ACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTG--TCAAG 1422
              || |||||||||||||||||||||||||||||||||||||| ||||| |||| |   |
Db        726 ACNACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTTAAACCCAGCCCGGTCAAGA 785

Qy       1423 AATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACAC 1465
              |||||||||||||||||||||||  ||   | || | | || |
Db        786 AATCTTTGAACACACATCCATGGGCAAACACCTTTAAATACCC 828


RESULT 7
BG218523
LOCUS       BG218523                831 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST38146 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG218523
VERSION     BG218523.1  GI:13744432
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 831)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 509.
FEATURES              Location/Qualifiers
     source           1. .831
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /cell_line="HT1080"
                      /clone_lib="Athersys RAGE Library"
                      /note="See 'Creation of Genome-wide Protein Expression
                      Libraries using Random Activation of Gene Expression',
                      Nature Biotechnology, in press. Note that even though the
                      cell type indicated is HT1080, since a random activation
                      method was used, these sequence tags are not necessarily
                      expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match             27.5%;  Score 762.4;  DB 12;  Length 831;
  Best Local Similarity   97.0%;  Pred. No. 1e-132;
  Matches  798;  Conservative    0;  Mismatches   22;  Indels    3;  Gaps    2;

Qy       1181 GGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGG 1240
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTAGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGG 60

Qy       1241 TTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTG 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTG 120

Qy       1301 CTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAG 1360
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Db        121 CTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAG 180

Qy       1361 AATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCA 1420

Db        181 AATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCA 240

Qy       1421 AGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAG 1480

Db        241 AGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAG 300

Qy       1481 TTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTT 1540

Db        301 TTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTT 360

Qy       1541 TTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAAC 1600

Db        361 TTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAAC 420

Qy       1601 ACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGT 1660

Db        421 ACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGT 480

Qy       1661 CACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGT 1720

Db        481 CACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGT 540

Qy       1721 GTAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTA 1780

Db        541 GTAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTA 600

Qy       1781 GCATTTCCGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTT 1840

Db        601 GCATTTCCGCATCCATGCCAACGAGTCACATATGGTAGGACTGGAGCCATAGTAAAGGTC 660

Qy       1841 GATTTACTTCTACCAACTAGTATATAAAGTACTAA-TTAAATGCTAACATAGGAAGTTAG 1899

Db        661 GTTTTACTTCTACCCACTAGTATATTAAGTACTAATTTTAATGCTAACATAGGAAAGTAG 720

Qy       1900 AAAATACTAATAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATAT 1959

Db        721 AAAATACTAATTACCTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATAT 780

Qy       1960 ATCAGAAAACTTTCAATATTGGTGACTACCTAAATGTGATTTT 2002

Db        781 ATC--AAAAACTTTCATAANGGTGACTACCTAAATGGGATTTT 821


RESULT 8
BF338835
LOCUS       BF338835               926 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  602036272F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184321
            5', mRNA sequence.
ACCESSION   BF338835
VERSION     BF338835.1  GI:11285254
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 926)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov

            Plate: LLAM9501  row: p  column: 18
            High quality sequence stop: 735.
FEATURES             Location/Qualifiers
     source          1. .926
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4184321"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn64"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             27.4%;  Score 758.6;  DB 10;  Length 926;
  Best Local Similarity   96.1%;  Pred. No. 5e-132;
  Matches  798;  Conservative    0;  Mismatches   30;  Indels    2;  Gaps    2;

Qy       1119 GAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAG 1178

Db          1 GAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAG 60

Qy       1179 AGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGA 1238

Db         61 AGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGA 120

Qy       1239 GGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTC 1298

Db        121 GGTTTCTGGGAATCTCCANTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTC 180

Qy       1299 TGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGA 1358

Db        181 TGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGA 240

Qy       1359 AGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGT 1418

Db        241 AGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGT 300

Qy       1419 CAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGG 1478

Db        301 CAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGG 360

Qy       1479 AGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAAT 1538

Db        361 AGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAAT 420

Qy       1539 TTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATA 1598

Db        421 TTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATA 480

Qy       1599 ACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAA 1658

Db        481 ACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAA 540

Qy       1659 GTCACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACT 1718

Db        541 GTCACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACT 600

Qy       1719 GTGTAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGAT 1778

Db        601 GTGTAGCCTGTGTATGACTTTTACTGAACACAGTTATG-TTTGAGGCAGCATGGGTTGAT 659

Qy       1779 TAGCATTTCCGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGG 1838

Db        660 TAGCATTTCCGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGG 719

Qy       1839 TTGATTTACTTCTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTA 1898

Db        720 TTGATTTACTTCTAACAAATAGTATCTTAAGTACTAATTACAGGCTACCATAGGAGGTT- 778
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Qy       1899 GAAAATACTAATAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAA 1948
             ||||||||||||||||||  |      |   | || ||   | |  |||
Db        779 GAAAATACTAATAACTTTATTATTCGGGAACTATACTCGGAGGCTAGTAA 828


RESULT 9
CD656678
LOCUS       CD656678                783 bp    mRNA    linear   EST 18-JUN-2003
DEFINITION  AGENCOURT_14556073 NIA Human H1 Embryonic Stem Cell cDNA Library
            (Long) Homo sapiens cDNA clone IMAGE:30427246 5', mRNA sequence.
ACCESSION   CD656678
VERSION     CD656678.1  GI:31897214
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 783)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
             cDNA Library Preparation: Yulan Piao and Minoru Ko
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC c           lone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM514  row: f  column: 23
            High quality sequence stop: 724.
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30427246"
                     /tissue_type="Embryonic Stem cells"
                     /cell_line="WA01"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library
                     (Long)"
                     /note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI;
                     This is a long-transcript enriched cDNA library (Genome
                     Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01
                     cell line .  Undifferentiated human ES cell line WA01/H1
                     was obtained from WiCell Research Institute, Inc.,
                     Madison, Wi, cultured according to their instructions, on
                     MEF feeders. They formed round colonies with defined edges
                     and were positive for alkaline phosphatase, SSEA-4, OCT3,
                     OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45.  They are
                     negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1,
                     TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days
                     after plating), the ES cells from 4 X 6cm dishes were
                     treated with 1 mg/ml collagenase, type IV
                     (Invitrogen/GIBCO) for 5-10 min and gently scraped off
                     with 5 ml pipette.  RNA was purified with TRIzol Reagent
                     from Invitrogen. Protocol ref:  Genome Res. 11: 1553-1558
                     (2001). [PMID:11544199]) Double-stranded cDNAs were
                     synthesized with an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT-3'] from
                     3.4g of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform
                     extraction, and separated from free linkers by
                     Centricon-100 column.  Then, the cDNAs were amplified by
                     long-range high fidelity PCR using Ex Taq polymerase
                     (Takara) with a primer Sal4-S for 25 cycles.  The products
                     were purified by phenol/chloroform extraction and
                     Centricon-100 column. The cDNAs were digested with SalI
                     and NotI enzymes and cloned into SalI/NotI site of
                     pCMV-SPORT6 plasmid vector. The average insert size is
                     about 3.6kb."
ORIGIN

  Query Match           26.4%;  Score 731.6;  DB 14;  Length 783;
  Best Local Similarity   98.3%;  Pred. No. 6.1e-127;
  Matches  760;  Conservative    0;  Mismatches   10;  Indels    3;  Gaps    2;

Qy       1182 GTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGT 1241
              ||  |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GTAATCCGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGT 62

Qy       1242 TTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGC 1301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 TTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGC 122

Qy       1302 TCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGA 1361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGA 182

Qy       1362 ATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAA 1421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAA 242

Qy       1422 GAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGT 1481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGT 302

Qy       1482 TATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTT 1541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTT 362

Qy       1542 TGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA 1601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA 422

Qy       1602 CCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC 1661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 CCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC 482

Qy       1662 ACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTG 1721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTG 542

Qy       1722 TAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAG 1781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 TAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAG 602

Qy       1782 CATTTCCGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTG 1841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 CATTTCCGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTG 662

Qy       1842 ATTTACTTCTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAA 1901
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        663 ATTTACTTCTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATANGAAGTTAGAA 722

Qy       1902 AATACTAATAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAAT 1954
              |||||||   |  |||  ||||||||||||||| ||||||||||||||||
Db        723 AATACTA--TAACTTTTATACTCAGCGATCTATTC-TCTGATGCTAAATAAAT 772


RESULT 10
AY416018
LOCUS       AY416018                918 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM5750 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY416018
VERSION     AY416018.1  GI:39771978
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 918)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 918)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .918
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>918
                     /locus_tag="HCM5750"
ORIGIN

  Query Match             25.6%;  Score 708.6;  DB 29;  Length 918;
  Best Local Similarity   82.7%;  Pred. No. 1.2e-122;
  Matches  759;  Conservative    0;  Mismatches  159;  Indels    0;  Gaps    0;

Qy        569 ATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAATCTGCTC 628
              ||||||||||||||||||||||||||||| |||||||| |||||||||||||||| ||||||
Db          1 ATGGCCAGAGAAGATTCCGTGAAGTGTTTGCGCTGCTTGCTCTACGCCCTCAACCTGCTC 60

Qy        629 TTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAAAT 688
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||| |||
Db         61 TTTTGGTTAATGTCCATCAGTGTCTTGGCAGTTTCTGCTTGGATGAGGGACTACCTGAAT 120

Qy        689 AATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTT 748
              |||||| | |||||||||||||||||| |||||||| ||||| ||||| || ||||||||
Db        121 AATGTTTTGACTTTAACTGCAGAAACAAGGGTAGAAGAAGCGGTCATCTTAACTTACTTC 180

Qy        749 CCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTA 808
              || |||||||| || |||||||||||||| ||||| |||||||||||| ||||| ||| |
Db        181 CCCGTGGTTCACCCCGTCATGATTGCTGTCTGCTGCTTCCTTATCATCGTGGGAATGCTG 240

Qy        809 GGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTG 868
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGATACTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGNNNNNNNNNNNNNNN 300

Qy        869 CTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACTTATG 928

Db        301 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy        929 GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTA 988
              || |||||||| |||||||||||||| |||||||||||||| |||||||||||| || |||
Db        361 GTGCCAGTACAGTGGTCAGATATGGTTACTTTGAAAGCCAGAATGACAAATTACGGCTTA 420

Qy        989 CCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAGAGTTTAAGTGCTGT 1048
              || || ||| | |||||||| || |||||||||| ||||||||||||||||||||||||||
Db        421 CCGAGGTATAGATGGCTTACACACGCTTGGAATTATTTTCAGAGAGAGTTTAAGTGCTGT 480

Qy       1049 GGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCC 1108
              ||||| || || |||||||||||||||||||||||||| |||||||||||| || || |||
Db        481 GGAGTGGTGTACTTCACTGACTGGTTGGAAATGACAGAAATGGACTGGCCTCCCGACTCC 540

Qy       1109 TGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGAC 1168
              |||||||| || || |||||||| || ||||| ||||| ||||||||||||||||||||||
Db        541 TGCTGTGTCAGGGAGTTCCCAGGGTGCTCCAAGCAGGCTCACCAGGAAGATCTCAGTGAC 600

Qy       1169 CTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTG 1228
              ||||| |||||||||||||||||| |||||||||||||||||||||||||||||||| ||
Db         601 CTTTACCAAGAGGGTTGTGGGAAGAAGATGTATTCCTTTTTGAGAGGAACCAAACAATTG 660

Qy       1229 CAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTC 1288
              || || || |||||||||||||||||||||| |||||||||||||||||||||||||||||
Db         661 CAAGTTCTAAGGTTTCTGGGAATCTCCATTGGTGTGACACAAATCCTGGCCATGATTCTC 720

Qy       1289 ACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATG 1348
              |||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||
Db         721 ACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGAACAGACCAAATG 780

Qy       1349 ATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAA 1408
              | ||  |||| ||||| |  |||||||| |||||||||  || || |||||||| |||
Db         781 CTATCTCTGAAAAATGATACGTCTCAGCACTTGTCATGTCATTCTGTGGAACTGTTAAAA 840

Qy       1409 CCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTT 1468
              ||||| || |||||  |||||||| || ||||| |||||||||||||| |||||||| |||
Db         841 CCAAGTCTTTCAAGGATCTTTGAGCATACATCAATGGCAAACAGCTTCAATACACATTTT 900

Qy       1469 GAGATGGAGGAGTTATAA 1486
              |||||||| || |||| |
Db         901 GAGATGGAAGAATTATGA 918


RESULT 11
BU688134/c
LOCUS       BU688134                703 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EC1-adx-p-17-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-adx-p-17-0-UI 3', mRNA sequence.
ACCESSION   BU688134
VERSION     BU688134.1  GI:23544635
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 703)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .703
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-adx-p-17-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EC1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
```

UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 25.2%; Score 697; DB 13; Length 703;
Best Local Similarity 100.0%; Pred. No. 1.9e-120;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2072 TTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTCAGTTCTGATAAT 2131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 TTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTCAGTTCTGATAAT 644

Qy       2132 GTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTAGCC 2191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 GTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTAGCC 584

Qy       2192 TTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTA 2251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 TTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTA 524

Qy       2252 TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC 2311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC 464

Qy       2312 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGAT 2371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGAT 404

Qy       2372 TCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACAC 2431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACAC 344

Qy       2432 TTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATAT 2491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATAT 284

Qy       2492 AAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAA 2551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAA 224

Qy       2552 CATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTA 2611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTA 164

Qy       2612 CACAGATTATTAAATTTTTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGC 2671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 CACAGATTATTAAATTTTTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGC 104

Qy       2672 ATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATG 2731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 ATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATG 44

Qy       2732 TGTCAATAAATATTTTCTAGAGAGTAAAAAAAAAAAA 2768
             ||||||||||||||||||||||||||||||||||||
Db         43 TGTCAATAAATATTTTCTAGAGAGTAAAAAAAAAAAA 7
```

RESULT 12

BG203659

```
LOCUS       BG203659                762 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST23047 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG203659
VERSION     BG203659.1  GI:13725346
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 468.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN
```

Query Match 25.0%; Score 690.8; DB 12; Length 762;
Best Local Similarity 95.5%; Pred. No. 2.8e-119;
Matches 722; Conservative 0; Mismatches 32; Indels 2; Gaps 1;

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Qy       1181 GGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGG 1240
             |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTAGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGG 60

Qy       1241 TTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTG 1300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTG 120

Qy       1301 CTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAG 1360
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        121 CTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAG 180

Qy       1361 AATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCA 1420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCA 240

Qy       1421 AGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAG 1480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAG 300

Qy       1481 TTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTT 1540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTT 360

Qy       1541 TTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAAC 1600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        361 TTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAAC 420

Qy       1601 ACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGT 1660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGT 480

Qy       1661 CACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGT 1720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGT 540

Qy       1721 GTAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTA 1780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTA 600

Qy       1781 GCATTTCCGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTT 1840
             ||  || |||||||||| ||||| |||||||||| |||||||||||||||||||| |
Db        601 GCCATTTCGCATCCATGGCAACGAATCACATATGGTAGGACTGGAGCCATAGTAAAGGGT 660

Qy       1841 GATTTA--CTTCTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTA 1898
             |  |||   |    |||||||   |  || || ||||||||||||||| ||||||| |
Db        661 GGATTAACTTCTACCCAACTATATTTAAAGGTCCTAATTAAATGCTAACCTAGGAAGGTT 720

Qy       1899 GAAAATACTAATAACTTTTATTACTCAGCGATCTAT 1934
                |||||||||||||||||||||||| ||||||||
Db        721 AGAAATACTAATAACTTTTATTACTCAACGATCTAT 756
```

RESULT 13
BX487248

LOCUS	BX487248 700 bp mRNA linear EST 04-SEP-2003
DEFINITION	DKFZp686P15255_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686P15255 5', mRNA sequence.
ACCESSION	BX487248
VERSION	BX487248.1 GI:31951683
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 700)
AUTHORS	Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE	EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
JOURNAL	Unpublished (2003)
COMMENT	Contact: MIPS MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available. This clone (DKFZp686P15255) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES	Location/Qualifiers
source	1. .700
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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="DKFZp686P15255"
	/dev_stage="adult"
	/lab_host="DH10B"
	/clone_lib="686 (synonym: hlcc3)"
	/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

ORIGIN

Query Match 24.7%; Score 682.8; DB 13; Length 700;
Best Local Similarity 99.1%; Pred. No. 9e-118;
Matches 695; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy        353 GGGAGAGGAAGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGC 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGAGAGGAAGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGC 60

Qy        413 GAAGAAGTTCCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGC 472
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAAGAAG-TCCCTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGC 119

Qy        473 GTGGGGCACCGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTG 532
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GTGGGGCACCGGGCCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTG 179

Qy        533 GTGAAAGGATGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAG 592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GTGAAAGGATGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAG 239

Qy        593 TGTCTGCGCTGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTG 652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TGTCTGCGCTGCCTGCTCTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTG 299

Qy        653 TTGGCAGTTTCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAA 712
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TTGGCAGTTTCTGCATGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAA 359

Qy        713 ACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATT 772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATT 419

Qy        773 GCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGA 832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGA 479

Qy        833 AATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTG 892
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        480 AATCTGTTGCTTCTTGCATGGTACTTTGGAAGTNTGCTTGTCATTTTCTGTGTAGAACTG 539

Qy        893 GCTTGTGGCGTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATG 952
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GCTTGTGGCGTNTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATG 599

Qy        953 GTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCAT 1012
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        600 GTCACTTTGAAAGCCAGGATGANCAATTATGGATTACCTAGATATCGGTGGCTTACTCAT 659

Qy       1013 GCTTGGAATTTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGT 1053
              |||||||||||||||||||||||||||||||||||||||||
Db        660 GCTTGGAATTTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGT 700
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RESULT 14
AY416017

LOCUS	AY416017 918 bp DNA linear GSS 12-DEC-2003
DEFINITION	Pan troglodytes HCM5750 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY416017
VERSION	AY416017.1 GI:39771977
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE	1 (bases 1 to 918)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 918)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

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            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .918
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>918
                     /locus_tag="HCM5750"
ORIGIN

  Query Match            23.9%;  Score 662.8;  DB 29;  Length 918;
  Best Local Similarity  72.3%;  Pred. No. 4.6e-114;
  Matches  664;  Conservative    0;  Mismatches  254;  Indels    0;  Gaps    0;

Qy        569 ATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAATCTGCTC 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAATCTGCTC 60

Qy        629 TTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAAAT 688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAAAT 120

Qy        689 AATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTT 748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTT 180

Qy        749 CCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTA 808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTA 240

Qy        809 GGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTG 868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGNNNNNNNNNNNNNN 300

Qy        869 CTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACTTATG 928

Db        301 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy        929 GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTA 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTA 420

Qy        989 CCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAGAGTTTAAGTGCTGT 1048
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAGAGNNNNNNNNNNNN 480

Qy       1049 GGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCC 1108

Db        481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 540

Qy       1109 TGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGAC 1168

Db        541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600

Qy       1169 CTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTG 1228
                                                    ||||||||||||||||||||
Db        601 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGAGAGGAACCAAACAACTG 660

Qy       1229 CAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTC 1288
              |||||||||||||    |||||| ||||||||||||||||||||||||||||||||||||
Db        661 CAGGTGCTGAGGTNNNTGGGAANCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTC 720

Qy       1289 ACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATG 1348
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Qy       1349 ATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAA 1408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1409 CCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTT 1468
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Db        841 CCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTT 900

Qy       1469 GAGATGGAGGAGTTATAA 1486
              |||||||||||| ||||||
Db        901 GAGATGGAGGAATTATAA 918


RESULT 15
BG538289
LOCUS       BG538289                826 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602566759F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691319 5',
            mRNA sequence.
ACCESSION   BG538289
VERSION     BG538289.1  GI:13530521
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 826)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1510  row: e  column: 16
            High quality sequence stop: 700.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4691319"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            23.2%;  Score 642.2;  DB 12;  Length 826;
  Best Local Similarity  94.3%;  Pred. No. 3.5e-110;
  Matches  742;  Conservative    0;  Mismatches   38;  Indels    7;  Gaps    7;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAAG 60

Qy       2043 CTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGT 2102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGT 120

Qy       2103 ATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATT 2162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 ATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATT 180

Qy       2163 TGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGTC 2222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGTC 240

Qy       2223 CTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATT 2282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATT 300

Qy       2283 ACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAA 2342
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Db        301 ACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAA 360

Qy       2343 TAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCC 2402
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Db        361 TAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCC 420

Qy       2403 AAATGAAGACTCTTTTTGACACTAAACACTTTTTAA-AAAGCTTATCTTTGCCTTCTCCA 2461
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        421 AAATGAAGACTCTTTTTGACACTAAACACTTTTTAACAAAGCTTATCTTTGCCTTCTCCA 480

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAA-AATAGTGTTCTTTTTC 2520
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        481 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAACAATAGTGTTCTTTTTC 540

Qy       2521 TCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTT 2580
             ||||||||| |||||||||||||||||||||||||||||||||||||||||||| | | |
Db        541 TCCAGAAAACTGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTAG-TAT 599

Qy       2581 ATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGT 2640
             |||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Db        600 ATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATATTTTTACCAAGAG 659

Qy       2641 ATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTA 2700
                 ||| |   |  ||  || |||||||| ||||||||||   ||| |  ||  |
Db        660 TATCAGTATATCCATTGAAATGGGAAAGTGCA-TTTACTGTATTAGGAGTA-TAGGTAAA 717

Qy       2701 TTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAAAA 2760
             |||||||||||||| |||||| || | |||||||||||||| |||||||||  ||||
Db        718 TTTCTCAGAATATGGCAAGAAACTT-AGATGTGTCAATAAATA-TTTCTAGAGATCAAAA 775

Qy       2761 AAAAAAA 2767
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Db        776 TAAAAGA 782

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Job time : 7172.47 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 05:21:56 ; Search time 191.781 Seconds
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8009.661 Million cell updates/sec

Title: US-09-830-328C-4
Perfect score: 2768
Sequence: 1 tcgacgccaccatttaaag.....tagagagtaaaaaaaaaaaa 2768

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	55.6	2.0	11049	4	US-10-204-708-22	Sequence 22, Appl
	2	54.8	2.0	640681	4	US-09-790-988-1	Sequence 1, Appli
	3	51.6	1.9	3095	6	5231168-1	Patent No. 5231168
	4	51	1.8	8093	4	US-10-204-708-31	Sequence 31, Appl
c	5	51	1.8	640681	4	US-09-790-988-1	Sequence 1, Appli
c	6	50.8	1.8	1864	4	US-09-468-265-4	Sequence 4, Appli
	7	49.6	1.8	11050	4	US-10-204-708-86	Sequence 86, Appl
	8	49	1.8	724	3	US-08-998-416-683	Sequence 683, App
c	9	49	1.8	8920	2	US-08-446-855A-1	Sequence 1, Appli
c	10	49	1.8	8920	3	US-09-150-741-1	Sequence 1, Appli
c	11	48.8	1.8	8654	1	US-08-920-812-6	Sequence 6, Appli
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c	14	48.8	1.8	8654	1	US-08-362-577C-6	Sequence 6, Appli
c	15	48.8	1.8	8654	2	US-08-920-828-6	Sequence 6, Appli
c	16	48.4	1.7	3600	3	US-08-894-731-1	Sequence 1, Appli
c	17	48	1.7	7786	4	US-09-790-988-2	Sequence 2, Appli
	18	48	1.7	19233	4	US-10-204-708-46	Sequence 46, Appl
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	22	47.2	1.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
	23	47.2	1.7	6113	4	US-10-204-708-14	Sequence 14, Appl
	24	46.6	1.7	2058	2	US-08-749-391-1	Sequence 1, Appli
	25	46.6	1.7	2058	3	US-09-390-200-1	Sequence 1, Appli
	26	46.2	1.7	8961	4	US-10-204-708-80	Sequence 80, Appl
	27	45.8	1.7	19124	2	US-08-487-826B-13	Sequence 13, Appl
	28	45.6	1.6	636	3	US-08-998-416-1137	Sequence 1137, Ap
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	31	45.6	1.6	10467	4	US-10-204-708-2	Sequence 2, Appli
	32	45.6	1.6	20674	4	US-09-641-638-651	Sequence 651, App
c	33	45.4	1.6	8961	4	US-10-204-708-80	Sequence 80, Appl
	34	45.2	1.6	5152	4	US-10-204-708-73	Sequence 73, Appl
	35	45	1.6	827	3	US-08-998-416-535	Sequence 535, App
c	36	45	1.6	4673	1	US-07-638-431-1	Sequence 1, Appli
c	37	45	1.6	4673	5	PCT-US92-00018-1	Sequence 1, Appli
	38	45	1.6	6070	4	US-10-204-708-10	Sequence 10, Appl
c	39	45	1.6	6182	4	US-10-204-708-87	Sequence 87, Appl
	40	45	1.6	6317	4	US-10-204-708-11	Sequence 11, Appl
	41	45	1.6	10640	4	US-09-417-485D-5	Sequence 5, Appli
c	42	44.6	1.6	732	3	US-08-998-416-1036	Sequence 1036, Ap
	43	44.4	1.6	10467	4	US-10-204-708-1	Sequence 1, Appli
c	44	44.2	1.6	860	3	US-08-998-416-287	Sequence 287, App
	45	44	1.6	6265	4	US-09-129-112-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-204-708-22
; Sequence 22, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 22
; LENGTH: 11049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-22

Query Match 2.0%; Score 55.6; DB 4; Length 11049;
Best Local Similarity 55.8%; Pred. No. 0.00015;
Matches 106; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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Qy       2601 GTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTATAGTATATTTATTTGAAAT 2660
             |    | |  | | |     || ||||| |||| |  | |||||   || || ||    |
Db       9879 GGTATAGAAAAAAAATTAATTTTAATTTGTTTATATTATTATAGGTGATATAGTTTGTAA 9938

Qy       2661 GGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAAAGA 2720
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Qy       2721 AAATTAAAAT 2730
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Db       9999 AATTAAATAT 10008

RESULT 2
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
;  APPLICANT: SHIGENOBU, SHUJI
;  APPLICANT:  WATANABE, HIDEMI
;  APPLICANT:  HATTORI, MASAHIRA
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
;  FILE REFERENCE: 081356/0159
;  CURRENT APPLICATION NUMBER: US/09/790,988
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: JP2000-107160
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 640681
;   TYPE: DNA
;   ORGANISM: Buchnera sp.
US-09-790-988-1

  Query Match              2.0%;  Score 54.8;  DB 4;  Length 640681;
  Best Local Similarity   47.6%;  Pred. No. 0.0042;
  Matches  233;  Conservative    0;  Mismatches  247;  Indels   10;  Gaps    2;

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Db      353270 TAAATAAAATAGTTTTATTTAAATTCTTTATCATATATTTTTAAAT------AGAATAC 353323

Qy        2295 CATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTG 2354
Db      353324 CTTTAAAAAATATGATACATACGAAAAATATTTCTTTTAATTTTTTATATATTTAATTT 353383

Qy        2355 CACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTC 2414
Db      353384 ATTAAAATATAATGCATTCATTACGTAATTGATTTCTTTATTCATACCTATTTGTTAGTT 353443

Qy        2415 TTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAAGCAAT 2474
Db      353444 TTTAAAAAAATAAAAAGATTTTATAAAAAAAATTTATCTATTTTAGAAATACATATAAT 353503

Qy        2475 AGTCTCCAAGTCAATATAAATTC----TACAGAAAATAGTGTTCTTTTTCTCCAGAAAAA 2530
Db      353504 TTTTTAAATATTACTTAAAATTGATATTACTTAAAATAATTTTTTATTTTTATTAGAATT 353563

Qy        2531 TGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGA 2590
Db      353564 AACATTAAGTATTGAATACATTTTGATATTTAATTAAAATTCAACATAAATTTTTTCTGA 353623

Qy        2591 TTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTATAGTATATT 2650
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Qy        2651 TATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAA 2710
Db      353684 TATTATTAAATGGTAAATCTCCTTTATTTTATATTAAATATTCTTTTTTTCATTGAAAAT 353743

Qy        2711 TATGGAAAGA 2720
Db      353744 TATAGAAAGA 353753

RESULT 3
5231168-1
;Patent No. 5231168
;    APPLICANT: DZIEGIEL, MORTEN;BORRE, MARTIN;JEPSEN, SOREN;
;VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.
;    TITLE OF INVENTION: MALARIA ANTIGEN
;    NUMBER OF SEQUENCES: 19
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/409,658
;      FILING DATE: 18-SEP-1989
;SEQ ID NO:1:
;      LENGTH: 3095
5231168-1

  Query Match              1.9%;  Score 51.6;  DB 6;  Length 3095;
  Best Local Similarity   45.7%;  Pred. No. 0.00079;
  Matches  341;  Conservative    0;  Mismatches  389;  Indels   16;  Gaps    4;

Qy        2014 AAAATATTCTTACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATT 2073
Db        2332 ATATTTTTCCAAAACATTTAAATAATTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2391

Qy        2074 TTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTCAGTTCTGATAATGT 2133
Db        2392 TATTAAATAAAATTTTTTTTCTTATTATATGTAACTAATATTATTTATTAATAAATATAT 2451

Qy        2134 TAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTAGCCTT 2193
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Qy        2194 TCCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTATT 2253
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Qy        2254 TAAATACTTAA---CCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATT 2310
Db        2572 ATAATAAATAAAATATAGAAACATTTACAGTATATTTTATAATCTGAAAGTATACATGTA 2631

Qy        2311 CAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGA 2370
Db        2632 ATAAAAAAATTTTCTGGCTTTATAATAATAAATAAGAAAATTATTATTTATGTATTATT 2691

Qy        2371 TTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACA 2430
Db        2692 TTAAGAAATATTATATATAATGATAATAAATGAAAGAAA----------GAAAAAAAAAA 2741

Qy        2431 CTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATA 2490
Db        2742 TTTTTTTATTATCATTTTTTTCATAAATATTATAAATAATTATTATATATAAATACTGGA 2801

Qy        2491 TAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATC--ATTA 2548
Db        2802 TAAATATTTATGTATATATTTATATATATACCATGTTGCCTTTTGGCATAAATGCAATAA 2861

Qy        2549 AAACATGTGACAATTTAGAGATTCTTTGTTTTAT-TTCACTGATTAATATACTGTGGCAA 2607
Db        2862 AAATATGAAACAATAAATCTATGTTCTGATTTATATTCTTAGGTAATAAAATTCATATAT 2921

Qy        2608 ATTACACAGATTATTAAATTTTTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAA 2667
Db        2922 ATTTTTTTTAATTTTAAATATTTTAAAACAAATGATATAATTAAAATTAAATAAGAAAAA 2981

Qy        2668 GTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAA 2727
Db        2982 GTAAGATTTTATAATGTCCATAAATTTTTTTTTTTTTAGTAGAATATATTTAAATAAA 3041

Qy        2728 AATGTGTCAATAAATATTTTCTAGAG 2753
Db        3042 TATATATTATTAAGTTATATTTATAG 3067

RESULT 4
US-10-204-708-31
; Sequence 31, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
```

; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 31
; LENGTH: 8093
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-31

Query Match 1.8%; Score 51; DB 4; Length 8093;
Best Local Similarity 43.0%; Pred. No. 0.0023;
Matches 249; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

Qy 2147 TATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAA 2206
Db 513 TAGTTAAGGGTTAATTTAAAATTTTTGGTTTATATTTTTTTTTTATTTAATGATTATATG 572

Qy 2207 GCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACC 2266
Db 573 ATGTAAATTAATTTTATTAATATTTTAAGTAAAATATATTGGAATTTTATAAAATGTATA 632

Qy 2267 ACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGT 2326
Db 633 AGATTTTAATATTTAAGGAATTGGGGTTAGAAAGTAGAAGTGGTTTTTAGGTTTTTTAGT 692

Qy 2327 CTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGT 2386
Db 693 TTTTTTTTTAAGTAATAAAGTTTTGTTGTGAATATTTAAAGTTATTGGGAAATTATCGGT 752

Qy 2387 ATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTA 2446
Db 753 AGATTTTTTTGTTTTTTTTTTTCGGTTTTTTATTATGTTGTTTTTTTAGATATGTAAGTT 812

Qy 2447 TCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAA 2506
Db 813 TATTTTATTAATTAAAATTTTAGTTTGATTATTTTTGATAAGTATTTAATCGATATGTAA 872

Qy 2507 TAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAG 2566
Db 873 TTTTTTTTTTGTTTTAAATATGTATAATAGGATAGAGTTTTTAAATTTGATTTAATTATT 932

Qy 2567 AGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAAT 2626
Db 933 AATTTTTGATTTATAAGTGTTATGGTGAGTTAATAGAATTTATTAATGTTTTTATTGTAT 992

Qy 2627 TTTTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTT 2686
Db 993 TTTATTAGTTAAATTTAGAAGGTTGGAATTAGTTTTTTTTATTTAGTATTTTGTTAGTTT 1052

Qy 2687 GTGTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATT 2725
Db 1053 GTTTAGTTTGTATTTTTAATTTTGTTTTTAATGGTAATT 1091

RESULT 5
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935

; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 1.8%; Score 51; DB 4; Length 640681;
Best Local Similarity 44.4%; Pred. No. 0.049;
Matches 338; Conservative 0; Mismatches 415; Indels 8; Gaps 3;

Qy 1907 TAATAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAA 1966
Db 518397 TTATATTTTTTACTATTTTTAAAAATGTTTTTATATATCTTAAGTATAATTATTTTAAAA 518338

Qy 1967 AACTTTCAATATTGGTGACTACCTAAATGTGATT---TTTGCTGGTTACTAAAATATTCT 2023
Db 518337 AAATTATATGATTATGATCATAAATATTTTGATTAAATTCATAAAATATTATTTTTTTTT 518278

Qy 2024 TACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATAT 2083
Db 518277 ACACACTTAACATTACTAGTCTTTTTAAGTTTTTTATCTTTCCATTCATTTAATGTGTAA 518218

Qy 2084 AAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAAC 2143
Db 518217 GTATTTAAAGTTAACGAATATATTTTTTTTTCTATCATTTTTGATAGCATTGAAAAAATT 518158

Qy 2144 CATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAAT 2203
Db 518157 ATTCGGTGTCTATTAATTAGCGTTTGATTAATAAAATCATCGCTAATAATAATTATTCTT 518098

Qy 2204 AAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTA 2263
Db 518097 AAATGTGTAAGACCTTTTTTAGAGTAATGATGAAATTGGCTATCGTCATAAATTTCAATA 518038

Qy 2264 ACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCT 2323
Db 518037 AATTTTATATTT--ATTTTAGATATTAAATATTTTTTTATTTTTTCTAGAGTCATTAATT 517980

Qy 2324 GGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACT 2383
Db 517979 GATATTATGTCCTTTTTATTAATAAAAAAAATAGATAAAATTTTTTTATGCTATTTTGAT 517920

Qy 2384 TGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGC 2443
Db 517919 AGTATTATATTGTATTTTTTGATAAATAAATTTTTTAAAAAAATGTAATTTTTAATTTTA 517860

Qy 2444 TTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGA 2503
Db 517859 AATTTTAACAATTTTTAAAAAATAATTCAATTATTTCACAGATTATTACTTTTTATAAGA 517800

Qy 2504 AAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATT 2563
Db 517799 TAATAATTTTCCTATAAAAATTTTTGATAATAACAGTATTATTAAAGATATTTG---AAT 517743

Qy 2564 TAGAGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTA 2623
Db 517742 AAAAAATACATTATTTTTGAGGTTTTTGAATGATATTTTTAAACTATAATAATTTTATGA 517683

Qy 2624 AATTTTTTTACAAGAGTATAGTATATTTATTTGAAATGGGA 2664

```
Db     517682 AAACATTATCATTGATATTAATATTTTTTTTTCTGAATGGA 517642


RESULT 6
US-09-468-265-4/c
; Sequence 4, Application US/09468265
; Patent No. 6379928
; GENERAL INFORMATION:
;  APPLICANT: Berka, Randy M
;  APPLICANT:  Cullen, Daniel
;  APPLICANT:  Gray, Gregory L
;  APPLICANT:  Hayenga, Kirk J
;  APPLICANT:  Lawlis, Virgil B
;  TITLE OF INVENTION: Heterologous Polypeptides Expressed in Filamentous Fungi, Process
;  TITLE OF INVENTION:  Making Same and Vectors for Making Same
;  FILE REFERENCE: A-42909-5
;  CURRENT APPLICATION NUMBER: US/09/468,265
;  CURRENT FILING DATE:  1999-12-10
;  PRIOR APPLICATION NUMBER: 08/484,384
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/284,942
;  PRIOR FILING DATE: 1994-08-02
;  PRIOR APPLICATION NUMBER: 07/413,010
;  PRIOR FILING DATE: 1989-09-25
;  PRIOR APPLICATION NUMBER: 07/163,219
;  PRIOR FILING DATE: 1988-02-26
;  PRIOR APPLICATION NUMBER: 06/882,224
;  PRIOR FILING DATE: 1986-07-07
;  PRIOR APPLICATION NUMBER: 06/771,374
;  PRIOR FILING DATE: 1985-08-29
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1864
;   TYPE: DNA
;   ORGANISM: Emericella nidulans
US-09-468-265-4

  Query Match             1.8%;  Score 50.8;  DB 4;  Length 1864;
  Best Local Similarity   44.3%;  Pred. No. 0.00093;
  Matches  411;  Conservative    0;  Mismatches  492;  Indels   25;  Gaps    4;

Qy       1842 ATTTACTTCTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAA 1901
Db       1614 AATTAAGAATAAAAAAAATTATCTCTAGATAATATTAAATATTTAGAAAATAAGATATAT 1555

Qy       1902 AATACTAATAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATAT 1961
Db       1554 ATTTGTAATCTCTTAGGAAGCTCTATCTATTCTTCTTAATAATCTTAATAATTTTTTATA 1495

Qy       1962 CAGAAAACTT----------TCAATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTA 2011
Db       1494 GAGCTTTATTATTCTCCTAGACTATTTTTTATAGTTTCTTAAGTAATTTATTCTTAGCTT 1435

Qy       2012 CTAAAATATTCTTACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGA 2071
Db       1434 AGTTATTATAATTAATAATATTATAATAAAGTTTAGTAACAGTTTCAAGGTCAACTATAT 1375

Qy       2072 TTTTTTGTATATAAGTCTGTGTTAAA-TCTGTATAATTCAGTCGATTTCAGTTCTGATAA 2130
Db       1374 TTATATATTTTAATTAATTAATTAAATTCTTTAGTATTACTAAGATTTAAGTTATACTTA 1315

Qy       2131 TGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTAGC 2190
Db       1314 GATAAATACTATTCTTTAATATTATTCAGTTTTAGTAGCTATTTTTTATATATTTTAAGT 1255

Qy       2191 CTTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTT 2250
Db       1254 TAATTATTGTCTACCCTGGCTAGTATATCTTATTTATAGTATAATAATATATCTAGGCAA 1195

Qy       2251 ATTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATT 2310
Db       1194 AGCTGCTAGCTTACCTAGTTAATATTTAAAATAAAATTAAAATAATTAAGTATATCTGTC 1135

Qy       2311 CAGAATGTAGTCTGGTCTTTAGGAAGTATTAAT------AAGAAAATTTGCACATAACTT 2364
Db       1134 TAATATATTTACTATTTATTAAAATATCTAATTATAGTAAAGTATAGTAGGTTTTTATAA 1075

Qy       2365 AGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACAC 2424
Db       1074 TTTATAATAATAATAAAATTTTTTAAACTTATAAGCTCTAATTTCTAAACTTTTAAGCTA 1015

Qy       2425 TAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACA--------AGAAGCAATAG 2476
Db       1014 TTAATAATTACTAATAATTTTTATTATAAATTTTATAATTATATTTTGCAGGGAGAGTTC 955

Qy       2477 TCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTG 2536
Db        954 TTAAATAATAAATATAAAAATATAGTACTTTATTATTATTATATTATAATAATATTTTTC 895

Qy       2537 TGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTAATA 2596
Db        894 TAGTAGTCTAGTTTAATATAAGAGCTTTAAAAATTATTTCTTAATTAGGATTAAATTATA 835

Qy       2597 TACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTATAGTATATTTATTTG 2656
Db        834 TAAAAATAGAAGTTATTATAAATATTTAATTTAGCTATTTAAACTAGGTATACTTCTTAA 775

Qy       2657 AAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGA 2716
Db        774 TCTATAAAAATTTAATAATTTTTTATATTAGAATAGTAAGTAGGTATATCAGGTCTAAGA 715

Qy       2717 AAGAAAATTAAAATGTGTCAATAAATAT 2744
Db        714 AGTTTTATATAAATTAATAAAAATTTAT 687


RESULT 7
US-10-204-708-86
; Sequence 86, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
;  TITLE OF INVENTION:  by Assessing DNA Methylation
;  FILE REFERENCE: 5013.1012
;  CURRENT APPLICATION NUMBER: US/10/204,708
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: PCT/EP01/03971
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: DE 10019058.8
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 86
;   LENGTH: 11050
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-86

  Query Match             1.8%;  Score 49.6;  DB 4;  Length 11050;
  Best Local Similarity   53.0%;  Pred. No. 0.007;
  Matches  106;  Conservative    0;  Mismatches   94;  Indels    0;  Gaps    0;

Qy       2568 GATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATT 2627
Db       4259 GTTGGTTTTGTTTTTTTTAATAGTAATTTTATTGGTAATTTTAAATTGAATTTTAATAAG 4318
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Qy      2628 TTTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTG 2687
Db      4319 TTTTTTCGGTTTTTTCGATAATTTTTTTGAAGTGATAAGAGTTAATATTTATTTAGTTTT 4378

Qy      2688 TGTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTT 2747
Db      4379 TTATTAGTTGTTAGTTATTATAAAAAAGAAATATTGTAAGGTTTAGTTAATTTAATTTTT 4438

Qy      2748 CTAGAGAGTAAAAAAAAAAA 2767
Db      4439 TTTAATATTTATGTAAAAAA 4458
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RESULT 8
US-08-998-416-683
; Sequence 683, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 683:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1453RP
US-08-998-416-683

Query Match 1.8%; Score 49; DB 3; Length 724;
Best Local Similarity 46.6%; Pred. No. 0.0015;
Matches 267; Conservative 0; Mismatches 295; Indels 11; Gaps 3;

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Qy      2199 TTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTATTTAAAT 2258
Db       149 TAAAGAAAAATGGAATTATTTGTGGCATCTTAATTTTTATTATTTAATTGATTATTATCT 208

Qy      2259 ACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGT 2318
Db       209 ATTTAACATAAAACATTTTAAAATGTTATAAAATAAATAAGAAATTACTTAT----AGAA 264

Qy      2319 AGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAA 2378
Db       265 TATTTATTAAATAGTATTTAATTTAATTTTAATATTAAATATACCATTTTTATTAATAAA 324

Qy      2379 GGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAA 2438
Db       325 TAGATTATTAAGTTTATTAATATTAAGTGATATATAATTTAATTTATATAAATTATTTAA 384

Qy      2439 AAAGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCT 2498
Db       385 TTTACTTCATTGATATATATAATTATTAAATGTACCTTTCATAATATTTATTTTTATTAG 444

Qy      2499 ACAGAAAATAGTGTTCTTT-----TTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACA 2553
Db       445 TCTAGTAATATTTCTATTTAATAGTCTACCCTTTAATTGGATATTACTACCTACTAAATA 504

Qy      2554 TGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACA 2613
Db       505 TTTACCTAATAATATATTATTAAGAATACTTAAATCTAATAATTTATTATCTAAAGTATA 564

Qy      2614 CAGATTATTAAATTTTTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCAT 2673
Db       565 TAAATTAATTAAATCTTTTTTATTATTAT--TTAAATTATTATTAATTAGTAAATTATAT 622

Qy      2674 TTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTG 2733
Db       623 TTATTTATTTTATTAACATAATTTTTTGATAATAATATATCATAATTAAATGGTAATTTA 682

Qy      2734 TCAATAAATATTTTCTAGAGAGTAAAAAAAAAA 2766
Db       683 TTAATAATTATCTTTAATGAATTTAATGATAAA 715
```

RESULT 9
US-08-446-855A-1/c
; Sequence 1, Application US/08446855A
; Patent No. 5849573
; GENERAL INFORMATION:
; APPLICANT: Stewart, Thomas S
; APPLICANT: Flores, Maria V
; APPLICANT: O'Sullivan, William J
; TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
; TITLE OF INVENTION: phosphate synthetase II
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 1100 No. 5849573th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,855A
; FILING DATE: 06-Jul-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29.009
; REFERENCE/DOCKET NUMBER: 47-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:

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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8920 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic
US-08-446-855A-1

  Query Match             1.8%;  Score 49;  DB 2;  Length 8920;
  Best Local Similarity   47.3%;  Pred. No. 0.0089;
  Matches  148;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy       2456 TCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCT 2515
Db       8920 TCTAGAATAAGGAAAAAAAAACATATATATATATATATATATATACATATATATAGTCCC 8861

Qy       2516 TTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTT 2575
Db       8860 TTTTGTATATACAGTTCCTCTTTTTTTTCGTTGAATTTTTAAAAAAATCATAACATTTA 8801

Qy       2576 GTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACA 2635
Db       8800 TAAATTATTATATAATTAAAAGAATTTATACATTTTAATGTTTATATATTTTTATTTTTT 8741

Qy       2636 AGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTT 2695
Db       8740 TTATAATTAATAAATTTATTAAAATTATAAAATTATTTGTAAATTGAAAAAACCATTTTG 8681

Qy       2696 GTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAG 2755
Db       8680 GTTTATACATATGAGTGAATAAATAAAATTTGTATATATAACAAAAATTTATAAAAAAAT 8621

Qy       2756 TAAAAAAAAAAAA 2768
Db       8620 AAATCAATATAAA 8608

RESULT 10
US-09-150-741-1/c
; Sequence 1, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
;  APPLICANT: Stewart et al.
;  TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
; Patent No. 6183996
;  TITLE OF INVENTION: Synthetase II
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/09/150,741
;  CURRENT FILING DATE: 1998-09-10
;  EARLIER APPLICATION NUMBER: PL6380
;  EARLIER FILING DATE: 1992-12-16
;  EARLIER APPLICATION NUMBER: AU93/00617
;  EARLIER FILING DATE: 1993-12-02
;  EARLIER APPLICATION NUMBER: 08/446,855
;  EARLIER FILING DATE: 1995-07-06
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 8920
;   TYPE: DNA
;   ORGANISM: Plasmodium falciparum
US-09-150-741-1

  Query Match             1.8%;  Score 49;  DB 3;  Length 8920;
  Best Local Similarity   47.3%;  Pred. No. 0.0089;
  Matches  148;  Conservative    0;  Mismatches  165;  Indels    0;  Gaps    0;

Qy       2456 TCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCT 2515
Db       8920 TCTAGAATAAGGAAAAAAAAACATATATATATATATATATATATACATATATATAGTCCC 8861

Qy       2516 TTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTT 2575
Db       8860 TTTTGTATATACAGTTCCTCTTTTTTTTCGTTGAATTTTTAAAAAAATCATAACATTTA 8801

Qy       2576 GTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACA 2635
Db       8800 TAAATTATTATATAATTAAAAGAATTTATACATTTTAATGTTTATATATTTTTATTTTTT 8741

Qy       2636 AGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTT 2695
Db       8740 TTATAATTAATAAATTTATTAAAATTATAAAATTATTTGTAAATTGAAAAAACCATTTTG 8681

Qy       2696 GTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAG 2755
Db       8680 GTTTATACATATGAGTGAATAAATAAAATTTGTATATATAACAAAAATTTATAAAAAAAT 8621

Qy       2756 TAAAAAAAAAAAA 2768
Db       8620 AAATCAATATAAA 8608

RESULT 11
US-08-920-812-6/c
; Sequence 6, Application US/08920812
; Patent No. 5763188
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,812
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8654 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Staphylococcus epidermidis
;      STRAIN:  Clinical Isolate SE-22
US-08-920-812-6

  Query Match             1.8%;  Score 48.8;  DB 1;  Length 8654;
  Best Local Similarity   47.4%;  Pred. No. 0.0099;
  Matches  179;  Conservative    0;  Mismatches  197;  Indels    2;  Gaps    1;
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Qy        2391 TGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTT 2450
Db        2499 TGTTTTAATTCTACAAAAAGAGAAGTAACATACAAAAAGAGTTTAAAAAGTGGGTATATT 2440

Qy        2451 TGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTAC--AGAAAATA 2508
Db        2439 AATATAACTAAAGGCTTATTGATAGATGAAAAAGTTGTTAAAAATCCTACTTCTAAATTA 2380

Qy        2509 GTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAG 2568
Db        2379 ATAAACATTTATATATAAAAAATGTTAGTAAAATTCTTTCCAAAAAGTATTCTTTTTAGT 2320

Qy        2569 ATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTT 2628
Db        2319 ATAATTTTTATTAAATTAAGGAAAATTAGAAACAATCTTATTTTTTTGAATATAGCAAAT 2260

Qy        2629 TTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGT 2688
Db        2259 GCTACATTGCTAATTCAAGTATAAACTTTAAAAGATAATTTGTTTTATAAACACTTATTT 2200

Qy        2689 GTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTC 2748
Db        2199 GTTTACTTCTTAATTTTATTTAGTTATAATTAACTAAATAATATAGCATTAAATATATTC 2140

Qy        2749 TAGAGAGTAAAAAAAAAA 2766
Db        2139 TTTAAATTTAAATTAATA 2122
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RESULT 12
US-08-920-827-6/c
; Sequence 6, Application US/08920827
; Patent No. 5770375
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,827
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-22
US-08-920-827-6

Query Match 1.8%; Score 48.8; DB 1; Length 8654;
Best Local Similarity 47.4%; Pred. No. 0.0099;
Matches 179; Conservative 0; Mismatches 197; Indels 2; Gaps 1;

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Qy        2391 TGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTT 2450
Db        2499 TGTTTTAATTCTACAAAAAGAGAAGTAACATACAAAAAGAGTTTAAAAAGTGGGTATATT 2440

Qy        2451 TGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTAC--AGAAAATA 2508
Db        2439 AATATAACTAAAGGCTTATTGATAGATGAAAAAGTTGTTAAAAATCCTACTTCTAAATTA 2380

Qy        2509 GTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAG 2568
Db        2379 ATAAACATTTATATATAAAAAATGTTAGTAAAATTCTTTCCAAAAAGTATTCTTTTTAGT 2320

Qy        2569 ATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTT 2628
Db        2319 ATAATTTTTATTAAATTAAGGAAAATTAGAAACAATCTTATTTTTTTGAATATAGCAAAT 2260

Qy        2629 TTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGT 2688
Db        2259 GCTACATTGCTAATTCAAGTATAAACTTTAAAAGATAATTTGTTTTATAAACACTTATTT 2200

Qy        2689 GTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTC 2748
Db        2199 GTTTACTTCTTAATTTTATTTAGTTATAATTAACTAAATAATATAGCATTAAATATATTC 2140

Qy        2749 TAGAGAGTAAAAAAAAAA 2766
Db        2139 TTTAAATTTAAATTAATA 2122
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RESULT 13
US-08-921-177-6/c
; Sequence 6, Application US/08921177
; Patent No. 5798211
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,177
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8654 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Staphylococcus epidermidis
;      STRAIN:  Clinical Isolate SE-22
US-08-921-177-6

  Query Match             1.8%;  Score 48.8;  DB 1;  Length 8654;
  Best Local Similarity   47.4%;  Pred. No. 0.0099;
  Matches  179;  Conservative    0;  Mismatches  197;  Indels    2;  Gaps    1;

Qy       2391 TGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTT 2450
Db       2499 TGTTTTAATTCTACAAAAAGAGAAGTAACATACAAAAAGAGTTTAAAAAGTGGGTATATT 2440

Qy       2451 TGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTAC--AGAAAATA 2508
Db       2439 AATATAACTAAAGGCTTATTGATAGATGAAAAAGTTGTTAAAAATCCTACTTCTAAATTA 2380

Qy       2509 GTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAG 2568
Db       2379 ATAAACATTTATATATAAAAAATGTTAGTAAAATTCTTTCCAAAAAGTATTCTTTTTAGT 2320

Qy       2569 ATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTT 2628
Db       2319 ATAATTTTTATTAAATTAAGGAAAATTAGAAACAATCTTATTTTTTTGAATATAGCAAAT 2260

Qy       2629 TTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGT 2688
Db       2259 GCTACATTGCTAATTCAAGTATAAACTTTAAAAGATAATTTGTTTTATAAACACTTATTT 2200

Qy       2689 GTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTC 2748
Db       2199 GTTTACTTCTTAATTTTATTTAGTTATAATTAACTAAATAATATAGCATTAAATATATTC 2140

Qy       2749 TAGAGAGTAAAAAAAAAA 2766
Db       2139 TTTAAATTTAAATTAATA 2122


RESULT 14
US-08-362-577C-6/c
; Sequence 6, Application US/08362577C
; Patent No. 5807673
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,577C
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8654 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Staphylococcus epidermidis
;      STRAIN:  Clinical Isolate SE-22
US-08-362-577C-6

  Query Match             1.8%;  Score 48.8;  DB 1;  Length 8654;
  Best Local Similarity   47.4%;  Pred. No. 0.0099;
  Matches  179;  Conservative    0;  Mismatches  197;  Indels    2;  Gaps    1;

Qy       2391 TGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTT 2450
Db       2499 TGTTTTAATTCTACAAAAAGAGAAGTAACATACAAAAAGAGTTTAAAAAGTGGGTATATT 2440

Qy       2451 TGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTAC--AGAAAATA 2508
Db       2439 AATATAACTAAAGGCTTATTGATAGATGAAAAAGTTGTTAAAAATCCTACTTCTAAATTA 2380

Qy       2509 GTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAG 2568
Db       2379 ATAAACATTTATATATAAAAAATGTTAGTAAAATTCTTTCCAAAAAGTATTCTTTTTAGT 2320

Qy       2569 ATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTT 2628
Db       2319 ATAATTTTTATTAAATTAAGGAAAATTAGAAACAATCTTATTTTTTTGAATATAGCAAAT 2260

Qy       2629 TTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGT 2688
Db       2259 GCTACATTGCTAATTCAAGTATAAACTTTAAAAGATAATTTGTTTTATAAACACTTATTT 2200

Qy       2689 GTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTC 2748
Db       2199 GTTTACTTCTTAATTTTATTTAGTTATAATTAACTAAATAATATAGCATTAAATATATTC 2140

Qy       2749 TAGAGAGTAAAAAAAAAA 2766
Db       2139 TTTAAATTTAAATTAATA 2122


RESULT 15
US-08-920-828-6/c
; Sequence 6, Application US/08920828
; Patent No. 5853998
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
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; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,828
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-22
US-08-920-828-6

Query Match 1.8%; Score 48.8; DB 2; Length 8654;
Best Local Similarity 47.4%; Pred. No. 0.0099;
Matches 179; Conservative 0; Mismatches 197; Indels 2; Gaps 1;

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Db       2499 TGTTTTAATTCTACAAAAAGAGAAGTAACATACAAAAAGAGTTTAAAAAGTGGGTATATT 2440

Qy       2451 TGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTAC--AGAAAATA 2508
                  |     ||      |   |     |    ||||   || |||| ||||    ||| ||
Db       2439 AATATAACTAAAGGCTTATTGATAGATGAAAAAGTTGTTAAAAATCCTACTTCTAAATTA 2380

Qy       2509 GTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAG 2568
               |   | |||       |||||| | || | | || ||  || | ||      |||
Db       2379 ATAAACATTTATATATAAAAAATGTTAGTAAAATTCTTTCCAAAAAGTATTCTTTTTAGT 2320

Qy       2569 ATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTT 2628
             ||  ||| | |||  |  |  ||  | || |      |  |||     || |||   |  |
Db       2319 ATAATTTTTATTAAATTAAGGAAAATTAGAAACAATCTTATTTTTTTGAATATAGCAAAT 2260

Qy       2629 TTTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGT 2688
                |    |   ||   |  | |  |  ||  |  ||  ||  || ||      || | |
Db       2259 GCTACATTGCTAATTCAAGTATAAACTTTAAAAGATAATTTGTTTTATAAACACTTATTT 2200

Qy       2689 GTATTTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTC 2748
             || |   |  ||| || |     |  | ||  ||    | ||| |  || |||||| |||
Db       2199 GTTTACTTCTTAATTTTATTTAGTTATAATTAACTAAATAATATAGCATTAAATATATTC 2140

Qy       2749 TAGAGAGTAAAAAAAAAA 2766
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Db       2139 TTTAAATTTAAATTAATA 2122
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Search completed: May 17, 2004, 08:41:27
Job time : 194.781 secs

OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 07:43:11 ; Search time 10751.2 Seconds
(without alignments)
11159.041 Million cell updates/sec

Title: US-09-830-328C-4
Perfect score: 2768
Sequence: 1 tcgacgccaccatttaaag.....tagagagtaaaaaaaaaaaa 2768

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		2550.4	92.1	2577	9	BC031265	BC031265 Homo sapi
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3		2393.8	86.5	2397	6	AX376256	AX376256 Sequence
4		2393.8	86.5	2397	6	AX697204	AX697204 Sequence
5		2393.8	86.5	2397	9	AY358703	AY358703 Homo sapi
6		2260.2	81.7	2267	9	AF124522	AF124522 Homo sapi
7		1788.6	64.6	1807	6	BD269117	BD269117 TM4SF rec
8	c	1582.2	57.2	143436	9	AC004456	AC004456 Homo sapi
9	c	1538	55.6	158789	2	AC146259	AC146259 Pan trogl
10	c	863.4	31.2	96782	9	AL592436	AL592436 Human DNA
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12		608.2	22.0	616	6	AX079479	AX079479 Sequence
13		596.4	21.5	251308	2	AC023234	AC023234 Mus muscu
14	c	572.2	20.7	188638	2	AC117109	AC117109 Rattus no
15	c	572.2	20.7	221680	2	AC116288	AC116288 Rattus no
16		414.4	15.0	442	6	BD061022	BD061022 Secreted
17		390.8	14.1	1683	5	BC054563	BC054563 Danio rer
18	c	383	13.8	383	6	AX332306	AX332306 Sequence
19	c	383	13.8	383	6	AX334593	AX334593 Sequence
20		323.4	11.7	425	6	AX193026	AX193026 Sequence
21		268.6	9.7	154134	10	AC122421	AC122421 Mus muscu
22		237.2	8.6	847	11	BV046235	BV046235 S212P6968
23		144	5.2	147	6	AX908771	AX908771 Sequence
24		144	5.2	147	6	BD044304	BD044304 Sequence
25	c	125.8	4.5	251308	2	AC023234	AC023234 Mus muscu
26		89.4	3.2	200582	5	AL929016	AL929016 Zebrafish
27		84.4	3.0	313050	3	PFA929352	AL929352 Plasmodiu
28		84.2	3.0	176898	9	AC117569	AC117569 Homo sapi
29	c	84.2	3.0	194028	2	AC111077	AC111077 Homo sapi
30		82	3.0	104853	9	AC117444	AC117444 Homo sapi
31	c	81	2.9	250029	3	AE014839	AE014839 Plasmodiu
32	c	80.2	2.9	8056	6	AX599046	AX599046 Sequence
33	c	80	2.9	30157	9	AC073242	AC073242 Homo sapi
34	c	79.8	2.9	349751	3	PFMAL4P3	AL035476 Plasmodiu
35	c	79.2	2.9	170305	9	AC007465	AC007465 Homo sapi
36	c	78.8	2.8	76568	3	MBREV	AF538053 Monosiga
37	c	78.6	2.8	8056	6	AX598900	AX598900 Sequence
38	c	77.8	2.8	158699	9	AP006183	AP006183 Homo sapi
39		76.6	2.8	1192	9	HSA323759	AJ323759 Homo sapi
40	c	76.4	2.8	199551	2	AC006281	AC006281 Plasmodiu
41		76.4	2.8	250531	3	AE014845	AE014845 Plasmodiu
42	c	76.2	2.8	155106	9	AC104069	AC104069 Homo sapi
43	c	76.2	2.8	258658	3	AE014832	AE014832 Plasmodiu
44	c	75.8	2.7	147114	9	BS000121	BS000121 Pan trogl
45	c	75.6	2.7	135121	9	AC069525	AC069525 Homo sapi

ALIGNMENTS

RESULT 1
BC031265
LOCUS BC031265 2577 bp mRNA linear PRI 07-OCT-2003
DEFINITION Homo sapiens transmembrane 4 superfamily member 12, mRNA (cDNA clone MGC:39733 IMAGE:5275953), complete cds.
ACCESSION BC031265
VERSION BC031265.1 GI:21411498
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2577)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 2577)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 63 Row: j Column: 1.

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REFERENCE   1
  AUTHORS   Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
            Wood,W.I.
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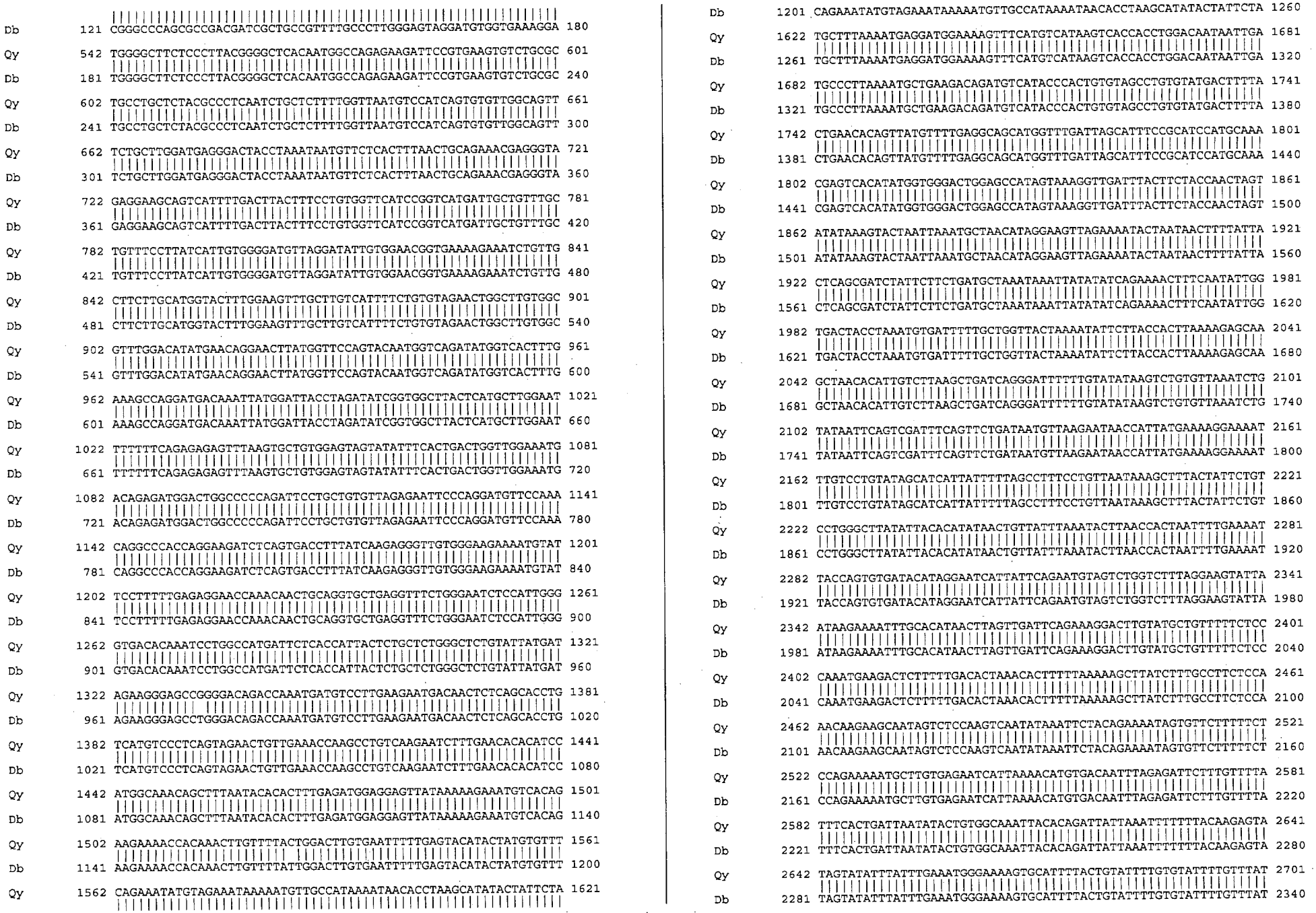
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RESULT 3
AX376256
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VERSION     AX376256.1  GI:19170519
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REFERENCE   1
  AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0168848-A 323 20-SEP-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          1 AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTT 60

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REFERENCE   1
  AUTHORS   Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
            Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
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  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0078961-A 272 28-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
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Query Match 86.5%; Score 2393.8; DB 6; Length 2397;
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Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
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Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
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Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
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Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
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Db       2041 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2100

Qy       2462 AACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCT 2521
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Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
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Qy       2582 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTA 2280

Qy       2642 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2701
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Db       2281 TAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTAT 2340

Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
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Db       2341 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2397
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RESULT 5
AY358703
LOCUS       AY358703               2397 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA68880 NET-2 (UNQ774) mRNA, complete cds.
ACCESSION   AY358703
VERSION     AY358703.1  GI:37182527
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2397)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 2397)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
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     gene            1. .2397
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     CDS             208. .1125
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ORIGIN

Query Match 86.5%; Score 2393.8; DB 9; Length 2397;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        482 CGGGCCCAGCGCCGACGATCGCTGCCGTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 541
Db        121 CGGGCCCAGCGCCGACGATCGCTGCCGTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGA 180

Qy        542 TGGGGCTTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGC 601
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Qy        662 TCTGCTTGGATGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTA 721
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Qy        722 GAGGAAGCAGTCATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGC 781
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Qy        782 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 841
Db        421 TGTTTCCTTATCATTGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTG 480

Qy        842 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 901
Db        481 CTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGC 540

Qy        902 GTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTG 961
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Qy        962 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 1021
Db        601 AAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAT 660

Qy       1022 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 1081
Db        661 TTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATG 720

Qy       1082 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 1141
Db        721 ACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA 780

Qy       1142 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 1201
Db        781 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTAT 840

Qy       1202 TCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGG 1261
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Qy       1262 GTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGAT 1321
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Qy       1382 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1441
Db       1021 TCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCC 1080

Qy       1442 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1501
Db       1081 ATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAG 1140

Qy       1502 AAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTT 1561
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Qy       1562 CAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA 1621
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Qy       1622 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGA 1681
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Qy       1742 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1801
Db       1381 CTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAA 1440

Qy       1802 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1861
Db       1441 CGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGT 1500

Qy       1862 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1921
Db       1501 ATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA 1560

Qy       1922 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGG 1981
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Qy       1982 TGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAA 2041
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Qy       2042 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 2101
Db       1681 GCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTG 1740

Qy       2102 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 2161
Db       1741 TATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAAT 1800

Qy       2162 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 2221
Db       1801 TTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT 1860

Qy       2222 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 2281
Db       1861 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAAT 1920

Qy       2282 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 2341
Db       1921 TACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTA 1980

Qy       2342 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2401
Db       1981 ATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCC 2040

Qy       2402 CAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCA 2461
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Qy       2522 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2581
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Db       2161 CCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTA 2220

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Qy       2702 TTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
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RESULT 6
AF124522

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LOCUS       AF124522               2267 bp    mRNA    linear   PRI 03-MAY-2000
DEFINITION  Homo sapiens tetraspan NET-2 mRNA, complete cds.
ACCESSION   AF124522
VERSION     AF124522.1  GI:4325291
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Serru,V., Dessen,P., Boucheix,C. and Rubinstein,E.
  TITLE     Sequence and expression of seven new tetraspans
  JOURNAL   Biochim. Biophys. Acta 1478 (1), 159-163 (2000)
  MEDLINE   20185353
   PUBMED   10719184
REFERENCE   2  (bases 1 to 2267)
  AUTHORS   Rubinstein,E., Serru,V., Dessen,P. and Boucheix,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-1999) INSERM U268, 14 Av Paul Vaillant Couturier,
            Villejuif 94807, France
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ORIGIN
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Qy        564 TCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAATC 623
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Qy        624 TGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACC 683
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Qy        684 TAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTT 743
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Qy        744 ACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGA 803
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Qy        804 TGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAA 863
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Qy        864 GTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAAC 923
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Db        361 GTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAAC 420

Qy        924 TTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATG 983
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Db        421 TTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATG 480

Qy        984 GATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAGAGTTTAAGT 1043
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Qy       1044 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAG 1103
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Db        541 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAG 600

Qy       1104 ATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCA 1163
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Qy       1164 GTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAAC 1223
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Db        661 GTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAAC 720

Qy       1224 AACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGA 1283
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Db        721 AACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGA 780

Qy       1284 TTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACC 1343
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Db        781 TTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACC 840

Qy       1344 AAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGT 1403
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Qy       1404 TGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACAC 1463
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Qy       1464 ACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTT 1523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTT 1020

Qy       1524 ACTGGACTTGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAA 1583
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATTGGACTTGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAA 1080

Qy       1584 TGTTGCCATAAAATAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAA 1643
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Db       1081 TGTTGCCATAAAATAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAA 1140

Qy       1644 AGTTTCATGTCATAAGTCACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACA 1703
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Db        1141 AGTTTCATGTCATAAGTCACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACA 1200

Qy        1704 GATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAG 1763
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Db        1201 GATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAG 1260

Qy        1764 GCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACATATGGTGGGACTG 1823
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Db        1321 GAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACTAATTAAATGC 1380

Qy        1884 TAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTCTTCTGAT 1943
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Db        1381 TAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTCTTCTGAT 1440

Qy        1944 GCTAAATAAATTATATATCAGAAAACTTTCAATATTGGTGACTACCTAAATGTGATTTTT 2003
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Db        1441 GCTAAATAAATTATATATCAGAAAACTTTCAATATTGGTGACTACCTAAATGTGATTTTT 1500

Qy        2004 GCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCTG 2063
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Qy        2244 AACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAAT 2303
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Qy        2364 TAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACA 2423
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RESULT 7
BD269117
LOCUS       BD269117                1807 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  TM4SF receptors.
ACCESSION   BD269117
VERSION     BD269117.1  GI:33078885
KEYWORDS    JP 2002543848-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1807)
  AUTHORS   Ruben,S.M., Ni,J., Fan,P., Roschke,V., Shi,Y., Komatsoulis,G.A. and
            Rosen,C.A.
  TITLE     TM4SF receptors
  JOURNAL   Patent: JP 2002543848-A 8 24-DEC-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002543848-A/8
            PD   24-DEC-2002
            PF   18-MAY-2000 JP 2000618481
            PR   19-MAY-1999 US    60/135122,03-JUN-1999 US    60/137797 PR
            11-JUN-1999 US    60/138573,18-AUG-1999 US    60/149447 PR
            28-JAN-2000 US    60/178770
            PI   STEVEN M RUBEN,JIAN NI,PING FAN,VIKTOR ROSCHKE,YANGGU SHI, PI
             GEORGE A KOMATSOULIS,CRAIG A ROSEN
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P7/02,
            PC   A61P9/10,
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            PC   C07K16/28,
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              TM4SF receptors
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   99.8%;  Pred. No. 0;
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Db           4 ACGAGTTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTCAGAGA 63

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Qy        1094 TGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAG 1153
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Qy        1154 GAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGA 1213
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Qy       1694 GCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAACACAGTT 1753

Db        724 GCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAACACAGTT 783

Qy       1754 ATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACATAT 1813

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Db       1144 GATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATA 1203

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Qy       2294 ACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTT 2353

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Qy       2354 GCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACT 2413

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Db       1444 CTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAAGCAA 1503

Qy       2474 TAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAATGC 2533

Db       1504 TAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAATGC 1563

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RESULT 8
AC004456/c
LOCUS       AC004456              143436 bp    DNA     linear   PRI 15-OCT-2003
DEFINITION  Homo sapiens PAC clone RP5-1100F23 from 7, complete sequence.
ACCESSION   AC004456
VERSION     AC004456.1  GI:2979597
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1^ (bases 1 to 143436)
  AUTHORS   Sulston,J.E. and Wilson,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
   PUBMED   9847074
REFERENCE   2  (bases 1 to 143436)
  AUTHORS   Antoniou,B. and Le,T.
  TITLE     The sequence of Homo sapiens PAC clone RP5-1100F23
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 143436)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-1998) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   4  (bases 1 to 143436)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-FEB-2000) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   5  (bases 1 to 143436)
  AUTHORS   Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-OCT-2003) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_DJ1100F23
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            NOTICE:  This sequence may not represent the entire insert of this
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clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu

SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at http://www.chori.org using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994).
The library is from one male donor.
The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP5-872F7. Actual start of this clone is at base position 1 of RP5-1100F23 actual end is at 143436 of RP5-1100F23. The orientation of this clone is unknown.

FEATURES Location/Qualifiers

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  Matches 1596;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

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Qy       1260 GGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATG 1319
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Db      14974 GGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATG 14915

Qy       1320 ATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACC 1379
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Db      14914 ATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACC 14855

Qy       1380 TGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACAT 1439
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Db      14854 TGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACAT 14795

Qy       1440 CCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCAC 1499
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Db      14794 CCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCAC 14735

Qy       1500 AGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGT 1559
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Db      14734 AGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGT 14675

Qy       1560 TTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTC 1619
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Db      14674 TTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTC 14615

Qy       1620 TATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATT 1679
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Db      14614 TATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATT 14555

Qy       1680 GATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTT 1739
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Db      14554 GATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTT 14495

Qy       1740 TACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCA 1799
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Db      14494 TACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCA 14435

Qy       1800 AACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTA 1859
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Db      14434 AACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTA 14375

Qy       1860 GTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTAT 1919
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Db      14374 GTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTAT 14315

Qy       1920 TACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATT 1979
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Db      14314 TACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATT 14255

Qy       1980 GGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGC 2039
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Db      14254 GGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGC 14195

Qy       2040 AAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATC 2099
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Db      14194 AAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATC 14135

Qy       2100 TGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA 2159
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Db      14134 TGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA 14075

Qy       2160 ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCT 2219
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Qy       2220 GTCCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAA 2279
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Qy       2280 ATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTAT 2339
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Db      13954 ATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTAT 13895

Qy       2340 TAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCT 2399
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Db      13894 TAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCT 13835

Qy       2400 CCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTC 2459
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Db      13834 CCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTC 13775

Qy       2460 CAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTT 2519
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Db      13774 CAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTT 13715

Qy       2520 CTCCAGAAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTT 2579
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Qy       2580 TATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAG 2639
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Db      13654 TATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAG 13595

Qy       2640 TATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTT 2699
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Db      13594 TATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTT 13535

Qy       2700 ATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 2758
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Db      13534 ATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA 13476


RESULT 9
AC146259/c
LOCUS       AC146259               158789 bp    DNA     linear   HTG 01-AUG-2003
DEFINITION  Pan troglodytes chromosome UNK clone RP43-28H17, *** SEQUENCING IN
            PROGRESS ***, 8 unordered pieces.
ACCESSION   AC146259
VERSION     AC146259.1  GI:33387212
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 158789)
  AUTHORS   Wilson,R.K.
  TITLE     The sequence of Pan troglodytes clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 158789)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
            Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT
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            ---------- Genome Center ----------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            ---------- Project Information ----------
            Center project name: C_PT028H17
            ----------------------------------------------
            ---------- Summary Statistics  ----------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 155793 bases at least Q40
            Consensus quality: 156306 bases at least Q30
            Consensus quality: 156616 bases at least Q20
            ----------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     5105: contig of 5105 bp in length
            *    5106     5205: gap of unknown length
            *    5206     8945: contig of 3740 bp in length
            *    8946     9045: gap of unknown length
            *    9046    16922: contig of 7877 bp in length
            *   16923    17022: gap of unknown length
            *   17023    31089: contig of 14067 bp in length
            *   31090    31189: gap of unknown length
            *   31190    53416: contig of 22227 bp in length
            *   53417    53516: gap of unknown length
            *   53517   104166: contig of 50650 bp in length
            *  104167   104266: gap of unknown length
            *  104267   157141: contig of 52875 bp in length
            *  157142   157241: gap of unknown length
            *  157242   158789: contig of 1548 bp in length.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9598"
                     /chromosome="UNK"
                     /clone="RP43-28H17"
     misc_feature    1. .5105
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     misc_feature    5206. .8945
                     /note="assembly_name:Contig11"
     misc_feature    9046. .16922
                     /note="assembly_name:Contig12"
     misc_feature    17023. .31089
                     /note="assembly_name:Contig13"
     misc_feature    31190. .53416
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     misc_feature    53517. .104166
                     /note="assembly_name:Contig15"
     misc_feature    104267. .157141
                     /note="assembly_name:Contig16"
     misc_feature    157242. .158789
                     /note="assembly_name:Contig7"
ORIGIN

  Query Match             55.6%;  Score 1538;  DB 2;  Length 158789;
  Best Local Similarity   97.7%;  Pred. No. 0;
  Matches 1582;  Conservative    0;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1140 AACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGT 1199
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Db      35637 AACATATCTAAAGTAATGTTGACCATGTATTTCTTTTACAGGGTTGTGGGAAGAAAATGT 35578

Qy       1200 ATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTG 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35577 ATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTG 35518

Qy       1260 GGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATG 1319
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Db      35517 GGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATG 35458

Qy       1320 ATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACC 1379
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Db      35457 ATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACC 35398

Qy       1380 TGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACAT 1439
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Db      35397 TGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACAT 35338

Qy       1440 CCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATGTCAC 1499
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Db      35337 CCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAATTATAAAAAGAAATGTCAC 35278

Qy       1500 AGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATACTATGTGT 1559
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Db      35277 AGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTGT 35218

Qy       1560 TTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTC 1619
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Db      35217 TTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTC 35158

Qy       1620 TATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATT 1679
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Db      35157 TATGCTTTAAAATAAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATT 35098

Qy       1680 GATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTT 1739
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Db      35097 GATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTTTGTAGCCTGTGTATGAATTT 35038

Qy       1740 TACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCA 1799
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Db      35037 TACTGAACACAGTTATGTTTTGAAGCAGCATGGTTTGATTAGCATTTCCTCATCCATGCA 34978

Qy       1800 AACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTA 1859
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Db      34977 AACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTA 34918

Qy       1860 GTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTAT 1919
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Db      34917 GTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTAT 34858

Qy       1920 TACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATT 1979
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Db      34857 TACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATT 34798

Qy       1980 GGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGC 2039
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Qy       2040 AAGCTAACACATTGTCTTAAGCTGATCAGGGAT-TTTTTGTATATAAGTCTGTGTTAAAT 2098
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Qy       2099 CTGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAA 2158
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Db      34677 CTGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAA 34618

Qy       2159 AATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTC 2218
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Db      34617 AATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAGAGCTTTACTGTTC 34558

Qy       2219 TGTCCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAA 2278
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Db      34557 TGTCCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAA 34498

Qy       2279 AATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTA 2338
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Db      34497 AATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTA 34438

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Qy       2399 TCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCT 2458

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Qy       2519 TCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTT 2578

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Qy       2639 GTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTT 2698

Db      34139 GTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTT 34080

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RESULT 10
AL592436/c
LOCUS AL592436 96782 bp DNA linear PRI 15-NOV-2001
DEFINITION Human DNA sequence from clone RP11-710N8 on chromosome 1, complete sequence.
ACCESSION AL592436
VERSION AL592436.7 GI:16973137
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 96782)
AUTHORS Ramsay,H.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Nov 16, 2001 this sequence version replaced gi:16151298.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP11-710N8 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-710N8 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-710N8 is at 1 in this sequence. The true left end of clone RP5-929G5 is at 94783 in this sequence.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-710N8"
/clone_lib="RPCI-11.3"
ORIGIN

Query Match 31.2%; Score 863.4; DB 9; Length 96782;
Best Local Similarity 79.5%; Pred. No. 1.4e-171;
Matches 1236; Conservative 0; Mismatches 266; Indels 53; Gaps 16;

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Qy        892 GGCTTGTGGCGTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATAT 951

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Qy        952 GGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA 1011

Db      35932 AGTCACTTTGAAAGCCAGAATGGCAAA-TATGACTTACCTGGATACCAGTGGCTTACTCA 35874

Qy       1012 TGCTTGGAATTTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTG 1071

Db      35873 TGGTTGGAA-AGTTTTCGGTGGGCATTTAAGTGTTGTGAAGTAGTATGTTTCAGTGACTG 35815

Qy       1072 GTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGG 1131

Db      35814 GTTGGAAATGACAGGGACGGACTAGCCCCCAGAATCCTGCTATGCTAGAGAATT------ 35761

Qy       1132 ATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAA 1191

Db      35760 --------------CCCACCAGGAAGATCTTAGTGACCTTTATCAAGAGGACTGTGGGAA 35715

Qy       1192 GAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAAT 1251

Db      35714 CAAAA-ATGTTTCCTTTTGAAAGGAACCAAACAATCACAAGTGCTAAGTTTTCTGGGAAT 35656

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Db      35655 TTCCATTAAAGTGACACAAA-CCTGGCCATGATTCTCACCACTACTTAACTCTGGGCTCT 35597

Qy       1312 GTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTC 1371

Db      35596 GTATTATGAGAGAAGGGAGCCTGAGATAGACCAAATGACATCCCTGAAG-----CACCTC 35542

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Db      35541 TCAGCAAC--TCATGTCACTCAGTAGAACTGTCCATACCAAGCTTGTCAAGGATCTTTGA 35484

Qy       1432 ACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGA 1491

Db      35483 ACATACATCCTTGGCAAACAACTTTAATACACCCTTTGAAATGGAGTAAATATTAA---G 35427

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Db      35426 AATGTCAAAGAAGGAAACCACAAACTTATTTTATTGGACTTGTGAATTTTTGAGTACACA 35367

Qy       1552 C-TATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCAT 1610

Db      35366 CTTAACTGTTACAGAAATTTGTAGAAATAAACATGTTGCTATAAAGGAATGCCTGGGCAT 35307

Qy       1611 ATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGG 1670
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Db      35306 ATAATTTTCTACCCTTATAAATGAAGA---AAAAAGTTTTCATATTATGTCACCAGCTGG 35250

Qy       1671 ACAATAATTGATG-CCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGT 1729

Db      35249 ACACTAATTGATGTCCTTTATAATACTGAGGACAGATTTAATACCCACTTTATAGCCTGT 35190

Qy       1730 GTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCG 1789

Db      35189 GTAAGATTTTTTACTGAACACAGTATGTTTTGAGGTGGCATGGTTTGATCAGCATTT-CT 35131

Qy       1790 CATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT 1849

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Db      35070 CTACCAGGTAGTATATAAAGTACCAATCAACTGCTAACATAAGAAAACAAACAGTAATAA 35011

Qy       1910 TAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAAC 1969

Db      35010 TGACTTTTATTCCTTGGCGATATATTCTTTTGAGTGTGAATAGATTACACAAAAGAAAAT 34951

Qy       1970 TTTCAATATTG------GTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCT 2023

Db      34950 TTTTAAGATTGGTGAATGTGAATACCTACATGTAATTTTTGCTGGTTAGTAAAATATTCT 34891

Qy       2024 TACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGA-TTTTTTGTATA 2082

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Qy       2083 TAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTCAGTTCTGATAATGTTAAGAATAA 2142

Db      34830 TAAGCCTGTGTTAAGTCTTTATAATTCAATAGATTTCAGTTTTTATAATGTTAATAATAA 34771

Qy       2143 CCATTATGAAAAGGA-AAATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTA 2201

Db      34770 CAATTGTAAAAAAGATAAATTTGTCCTGTAAAGCACCATTATTTTTAGCCTTTCCTGTTA 34711

Qy       2202 ATAAAGCTTTACTATTCTGTCCTGGGCTTATAT-----TACACATATAACTGTTATTTAA 2256

Db      34710 ATGGAGCTTTAAAATTCTGTTTTGGGTTTATATAATAGCATATACATAACTATGAATTCA 34651

Qy       2257 ATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAAT 2316

Db      34650 AATACTTAACCACTAATTTGAAAATTATCAGTGTGATACACAGGAATCATTATTCAGAAT 34591

Qy       2317 GTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGA 2376

Db      34590 GTGGTCTGGTCTCTAGGAAGTATTAACAGGAAAGTTACCACACAATTTAGTTGATTTAGC 34531

Qy       2377 AAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACAC 2431

Db      34530 AAAGACCTAGATGCTATTTTTCTCCCAAACTAAGATACTTTTTGACACTAAACAC 34476
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LOCUS       AP001393               208942 bp    DNA     linear   HTG 03-APR-2003
DEFINITION  Homo sapiens chromosome 1 clone RP11-722J12 map 1p13, WORKING DRAFT
            SEQUENCE, 19 unordered pieces.
ACCESSION   AP001393
VERSION     AP001393.2  GI:8117304
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA of 1p
  JOURNAL   Published Only in Database (2000)
REFERENCE   2  (bases 1 to 208942)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-2000) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     On May 30, 2000 this sequence version replaced gi:7259334.
            -------------- Genome Center
                Center: RIKEN Genomic Sciences Center(GSC)
                Center code: RIKEN
                Web site: http://hgp.gsc.riken.go.jp/
                Contact: hattori@gsc.riken.go.jp
            -------------- Project Information
                Center project name: HumDraft 1
                Center clone name: RP11-722J12
            -------------- Summary Statistics
                Sequencing vector: PCR products; 100% of reads
                Chemistry: Dye-terminator ET-amersham; 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 185564 bases at least Q40
                Consensus quality: 199124 bases at least Q30
                Consensus quality: 204363 bases at least Q20
                Insert size: 207142; sum-of-contigs
                Quality coverage: 4.13x in Q20 bases; sum-of-contigs
            --------------.
            NOTE: This is a 'working draft' sequence. It currently consists of
            19 contigs. The true order of the pieces is not known and their
            order in this sequence record is arbitrary. Gaps between the
            contigs are represented as runs N, but the exact sizes of the gaps
            are unknown. This record will be updated with the finished sequence
            as soon as it is available and the accession number will be
            preserved
                  1     39924 contig of  39924 bp in length
              40025     59448 contig of  19424 bp in length
              59549     75185 contig of  15637 bp in length
              75286     90161 contig of  14876 bp in length
              90262    102243 contig of  11982 bp in length
             102344    114429 contig of  12086 bp in length
             114530    125315 contig of  10786 bp in length
             125416    137713 contig of  12298 bp in length
             137814    147894 contig of  10081 bp in length
             147995    156594 contig of   8600 bp in length
             156695    165511 contig of   8817 bp in length
             165612    172480 contig of   6869 bp in length
             172581    182109 contig of   9529 bp in length
             182210    187931 contig of   5722 bp in length
             188032    193656 contig of   5625 bp in length
             193757    199153 contig of   5397 bp in length
             199254    203762 contig of   4509 bp in length
             203863    207517 contig of   3655 bp in length
             207618    208942 contig of   1325 bp in length.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 19 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     39924: contig of 39924 bp in length
            *   39925     40024: gap of 100 bp
            *   40025     59448: contig of 19424 bp in length
            *   59449     59548: gap of 100 bp
            *   59549     75185: contig of 15637 bp in length
            *   75186     75285: gap of 100 bp
            *   75286     90161: contig of 14876 bp in length
            *   90162     90261: gap of 100 bp
            *   90262    102243: contig of 11982 bp in length
            *  102244    102343: gap of 100 bp
            *  102344    114429: contig of 12086 bp in length
            *  114430    114529: gap of 100 bp
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     *   114530    125315: contig of 10786 bp in length
     *   125316    125415: gap of 100 bp
     *   125416    137713: contig of 12298 bp in length
     *   137714    137813: gap of 100 bp
     *   137814    147894: contig of 10081 bp in length
     *   147895    147994: gap of 100 bp
     *   147995    156594: contig of 8600 bp in length
     *   156595    156694: gap of 100 bp
     *   156695    165511: contig of 8817 bp in length
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     *   165612    172480: contig of 6869 bp in length
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     *   172581    182109: contig of 9529 bp in length
     *   182110    182209: gap of 100 bp
     *   182210    187931: contig of 5722 bp in length
     *   187932    188031: gap of 100 bp
     *   188032    193656: contig of 5625 bp in length
     *   193657    193756: gap of 100 bp
     *   193757    199153: contig of 5397 bp in length
     *   199154    199253: gap of 100 bp
     *   199254    203762: contig of 4509 bp in length
     *   203763    203862: gap of 100 bp
     *   203863    207517: contig of 3655 bp in length
     *   207518    207617: gap of 100 bp
     *   207618    208942: contig of 1325 bp in length.
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                     /db_xref="taxon:9606"
                     /chromosome="1"
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                     /clone="RP11-722J12"
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     misc_feature    75286..90161
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  Matches 1235;  Conservative    0;  Mismatches  267;  Indels   53;  Gaps   16;

Qy        892 GGCTTGTGGCGTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATAT 951
Db      58441 GGCTAGTGGCATTTGGACATATGAACAGAAGTGTGTGGTTCCAGTACAGTGGTTAGATGT 58382

Qy        952 GGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA 1011
Db      58381 AGTCACTTTGAAAGCCAGAATGGCAAA-TATGACTTACCTGGATACCAGTGGCTTACTCA 58323

Qy       1012 TGCTTGGAATTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTAGTATATTTCACTGACTG 1071
Db      58322 TGGTTGGAA-AGTTTTCGGTGGGCATTTAAGTGTTGTGAAGTAGTATGTTTCAGTGACTG 58264

Qy       1072 GTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTTAGAGAATTCCCAGG 1131
Db      58263 GTTGGAAATGACAGGGACGGACTAGCCCCCAGAATCCTGCTATGCTAGAGAATT------ 58210

Qy       1132 ATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAA 1191
Db      58209 --------------CCCACCAGGAAGGTCTTAGTGACCTTTATCAAGAGGACTGTGGGAA 58164

Qy       1192 GAAAATGTATTCCTTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAAT 1251
Db      58163 CAAAA-ATGTTTCCTTTTGAAAGGAACCAAACAATCACAAGTGCTAAGTTTTCTGGGAAT 58105

Qy       1252 CTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCT 1311
Db      58104 TTCCATTAAAGTGACACAAA-CCTGGCCATGATTCTCACCACTACTTAACTCTGGGCTCT 58046

Qy       1312 GTATTATGATAGAAGGGAGCCGGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTC 1371
Db      58045 GTATTATGAGAGAAGGGAGCCTGAGATAGACCAAATGACATCCCTGAAG-----CACCTC 57991

Qy       1372 TCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGA 1431
Db      57990 TCAGCAAC--TCATGTCACTCAGTAGAACTGTCCATACCAAGCCTGTCAAGGATCTTTGA 57933

Qy       1432 ACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGA 1491
Db      57932 ACATACATCCTTGGCAAACAACTGTAATACACCCTTTGAAATGGAGTAAATATTAA---G 57876

Qy       1492 AATGTCACAGAAGAAAACCACAAACTTGTTTTACTGGACTTGTGAATTTTTGAGTACATA 1551
Db      57875 AATGTCAAAGAAGGAAACCACAAACTTATTTTATTGGACTTGTGAATTTTTGAGTACACA 57816

Qy       1552 C-TATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCAT 1610
Db      57815 CTTAACTGTTACAGAAATTTGTAGAAATAAACATGTTGCTATAAAGGAATGCCTGGGCAT 57756

Qy       1611 ATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGG 1670
Db      57755 ATAATTTTCTACCCTTATAAATGAAGA---AAAAAGTTTCATATTATGTCACCAGCTGG 57699

Qy       1671 ACAATAATTGATG-CCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGT 1729
Db      57698 ACACTAATTGATGTCCTTTATAATACTGAGGACAGATTTAATACCCACTTTATAGCCTGT 57639

Qy       1730 GTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCG 1789
Db      57638 GTAAGATTTTTTACTGAACACAGTATGTTTTGAGGTGGCATGGTTTGATCAGCATTT-CT 57580

Qy       1790 CATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT 1849
Db      57579 CATCCATGTAAATAAGCCACATATGGCGGGACTGGAACTACAGTAAATGTTAGTTTACTT 57520

Qy       1850 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAA 1909
Db      57519 CTACCAGGTAGTATATAAAGTACCAATCAACTGCTAACATAAGAAAACAAACAGTAATAA 57460

Qy       1910 TAACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAAC 1969
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Db      57459 TGACTTTTATTCCTTGGCGATATATTCTTTTGAGTGTGAATAGATTACACAAAAGAAAAT 57400

Qy       1970 TTTCAATATTG------GTGACTACCTAAAATGTGATTTTTGCTGGTTACTAAAATATTCT 2023

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Qy       2202 ATAAAGCTTTACTATTCTGTCCTGGGCTTATAT-----TACACATATAACTGTTATTTAA 2256

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Qy       2257 ATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAAT 2316

Db      57099 AATACTTAACCACTAATTTGAAAATTATCAGTGTGATACACAGGAATCATTATTCAGAAT 57040

Qy       2317 GTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGA 2376

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LOCUS       AX079479                 616 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 223 from Patent WO0107611.
ACCESSION   AX079479
VERSION     AX079479.1  GI:13159039
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Goddard,A. and Wood,W.I.
  TITLE     Human polypeptides and methods for the use thereof
  JOURNAL   Patent: WO 0107611-A 223 01-FEB-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   99.2%;  Pred. No. 7.5e-118;
  Matches  610;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        388 CCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTGCCCCGATGAGCCCCCGCCGTG 447

Db          2 CCAATGCAGCCCTCCGGTTNTCCGCGAAGAAGTTCCTTGCCCCGATGAGCCCCCGCCGTG 61

Qy        448 CGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCCAGCGCCGACGATCGCTGCC 507

Db         62 CGTCCCCGATTATCCCCAGGCGGGCGTGGGGCACCGGGCCCAGCGCCGACGATCGCTGCC 121

Qy        508 GTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTTACGGGGCTCAC 567

Db        122 GTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTTACGGGGCTCAC 181

Qy        568 AATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAATCTGCT 627

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Qy        628 CTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAAA 687

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Qy        688 TAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTT 747

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Qy        748 TCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTT 807

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Qy        808 AGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTT 867

Db        422 AGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTT 481

Qy        868 GCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACTTAT 927

Db        482 GCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACTTAT 541

Qy        928 GGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATT 987

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Qy        988 ACCTAGATATCGGTG 1002

Db        602 ACCTAGATATCGGTG 616
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LOCUS       AC023234               251308 bp    DNA     linear   HTG 15-MAY-2002
DEFINITION  Mus musculus chromosome 6 clone RP23-23N7 strain C57BL6/J, WORKING
            DRAFT SEQUENCE, 46 unordered pieces.
ACCESSION   AC023234
VERSION     AC023234.14  GI:15143449
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 251308)
  AUTHORS   Han,J., Montgomery,K.T., Grills,G., Lee,E., Long,J., Pomerantz,R.,
            Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
            Gordon,M., Goltz,J.S. and Kucherlapati,R.
  TITLE     High Throughput Mouse Sequencing
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 251308)
  AUTHORS   Han,J., Montgomery,K.T., Grills,G., Lee,E., Long,J., Pomerantz,R.,
            Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
            Gordon,M., Goltz,J.S. and Kucherlapati,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-2000) Department of Molecular Genetics, Albert
            Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
            Bronx, NY 10461, USA
COMMENT     On Aug 9, 2001 this sequence version replaced gi:14718674.
            ----------------Genome Center
            Center:  Harvard Partners Genome Center
            Center Code:  HPGC
            Web site: http://www.hpcgg.org/Sequence/mouse.html
            Contact: hpgc@mendel.mgh.harvard.edu
            ----------------Summary Statistics
            Center project name:  ABB
            Sequencing vector:  pUC18; L08752
            Chemistry:  Dye-terminator Big Dye; 100%
            *Consensus quality:  233188 at least Q20
            *Consensus quality:  225718 at least Q30
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*Consensus quality:  215659 at least Q40
Estimated insert size:   agarose-FP - N/A
**Estimated insert size: 250408 - sum-of-contigs
Quality coverage:  agarose-FP - N/A
Quality coverage:  5.8 x in Q20 bases; sum-of-contigs estimation
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 46 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*   116204   145659: contig of 29456 bp in length
*   145660   145679: gap of unknown length
*   145680   165843: contig of 20164 bp in length
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*   165864   177940: contig of 12077 bp in length
*   177941   177960: gap of unknown length
*   177961   185743: contig of 7783 bp in length
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*   185764   192691: contig of 6928 bp in length
*   192692   192711: gap of unknown length
*   192712   195875: contig of 3164 bp in length
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*   195896   199067: contig of 3172 bp in length
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*   201572   203436: contig of 1865 bp in length
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*   203457   206090: contig of 2634 bp in length
*   206091   206110: gap of unknown length
*   206111   208009: contig of 1899 bp in length
*   208010   208029: gap of unknown length
*   208030   210076: contig of 2047 bp in length
*   210077   210096: gap of unknown length
*   210097   211779: contig of 1683 bp in length
*   211780   211799: gap of unknown length
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*   216099   217834: contig of 1736 bp in length
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*   218921   221278: contig of 2358 bp in length
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*   221299   222674: contig of 1376 bp in length
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*   222695   224244: contig of 1550 bp in length
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*   231657   232776: contig of 1120 bp in length
*   232777   232796: gap of unknown length
*   232797   234440: contig of 1644 bp in length
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*   242238   242257: gap of unknown length
*   242258   244099: contig of 1842 bp in length
*   244100   244119: gap of unknown length
*   244120   245298: contig of 1179 bp in length
*   245299   245318: gap of unknown length
*   245319   246864: contig of 1546 bp in length
*   246865   246884: gap of unknown length
*   246885   248157: contig of 1273 bp in length
*   248158   248177: gap of unknown length
*   248178   249287: contig of 1110 bp in length
*   249288   249307: gap of unknown length
*   249308   250343: contig of 1036 bp in length
*   250344   250363: gap of unknown length
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Best Local Similarity   69.7%;  Pred. No. 3.9e-115;
Matches 1119;  Conservative    0;  Mismatches  411;  Indels   76;  Gaps   20;

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Db      57107 CTATCTCTGAAAAATGATACGTCTCAGCACTTGTCATGTCATTCTGTGGAACTGTTAAAA 57166

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Qy       1469 GAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTACTGG 1528
Db      57227 GAGATGGAAGAATTATGAA---GAATGTCAAAGAAGGAAATCACAAACTTGT-----GGG 57278

Qy       1529 ACTTGTGAATTTTTGAGTACATA-CTATGTGTTTCAGAAATATGTAGAAATAAAAATGTT 1587
Db      57279 ACTAGTGGGTTTTGGGGTACACAGTTATCTATTTCAGAAATTTTTAGACATATTAATATT 57338

Qy       1588 GCCATAAAATAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTT 1647
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Qy       1648 TCATGTCATAAGTCACCACCTGGACAATAATTGATGCCCTT-AAAATGCTGAAGACAGAT 1706
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Qy       1762 AGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACAT---ATGGTGG 1818
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Qy       1819 GACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACTAATTA 1878
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Qy       1939 CTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGGTGACTACCTAAATGTGA 1998
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Qy       1999 TTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCA--AGCTAACACATTGTCT 2056
Db      57735 TTTTTGTTGGTTACTAAAATAATCTTATTAATAACACTTGTAAGAGCTAACATGTTGTCT 57794

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Qy       2116 TTTCAGTTCTGATAATGTTAAGAATAAC--CATTATGAAAAGGAAAATTTGTCCTGTATA 2173
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Qy       2234 TTACACATATAACTGTT-ATTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGA 2292
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Qy       2293 TACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATT 2352
Db      58034 CACATAGGAATC---------TCTGTAAGTCTGGCTGCCGGAAGTATTAACTACAGAATT 58084

Qy       2353 TGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGAC 2412
Db      58085 TACACA-----TAGTTGATTCATCAAAAGTTCAGATTTTTCCCCCCTCCCAAAAAAACACT 58139

Qy       2413 TCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAAGCA 2472
Db      58140 TTGTCAAAGAGTGTTTTTCGTTTTTATTTTAATGTTTTCATGTATTTCTTTTGCAATCA 58199

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Db      58260 CTCATAGGAATCTCTAAAATAAGTGGTAGCCTAACCAGAGAAAATTCTTGATTTCTTTCA 58319

Qy       2587 CTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTATAGTA 2646
Db      58320 TCAATTAATACACTGTAGCAAATGATGCAGAATATT-AATTTTTTTACAAGAGTAGAAGA 58378

Qy       2647 TATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTC 2706
Db      58379 TATTTATTTGAAACGGGAAAAGTGCATTTTACTGTATCTTGTGCATTCTGTTCATTTCTT 58438

Qy       2707 AGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGA 2752
Db      58439 GGATTACAGAAAGAAAATTAA------TCAATAAATATTTTCTAGA 58478

RESULT 14
AC117109/c
LOCUS       AC117109               188638 bp    DNA     linear   HTG 15-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-242N20, *** SEQUENCING IN PROGRESS
            ***, 7 unordered pieces.
ACCESSION   AC117109
VERSION     AC117109.4  GI:25013238
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 188638)
```

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 188638)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (08-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 188638)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 15, 2002 this sequence version replaced gi:23194558.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
-------------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-------------- Project Information
Center project name: GTNB
Center clone name: CH230-242N20
-------------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 171601 bases at least Q40
Consensus quality: 173679 bases at least Q30
Consensus quality: 175403 bases at least Q20
Estimated insert size: 173126; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 11978: contig of 11978 bp in length
* 11979 12078: gap of unknown length
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* 166387 176280: contig of 9894 bp in length
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FEATURES Location/Qualifiers

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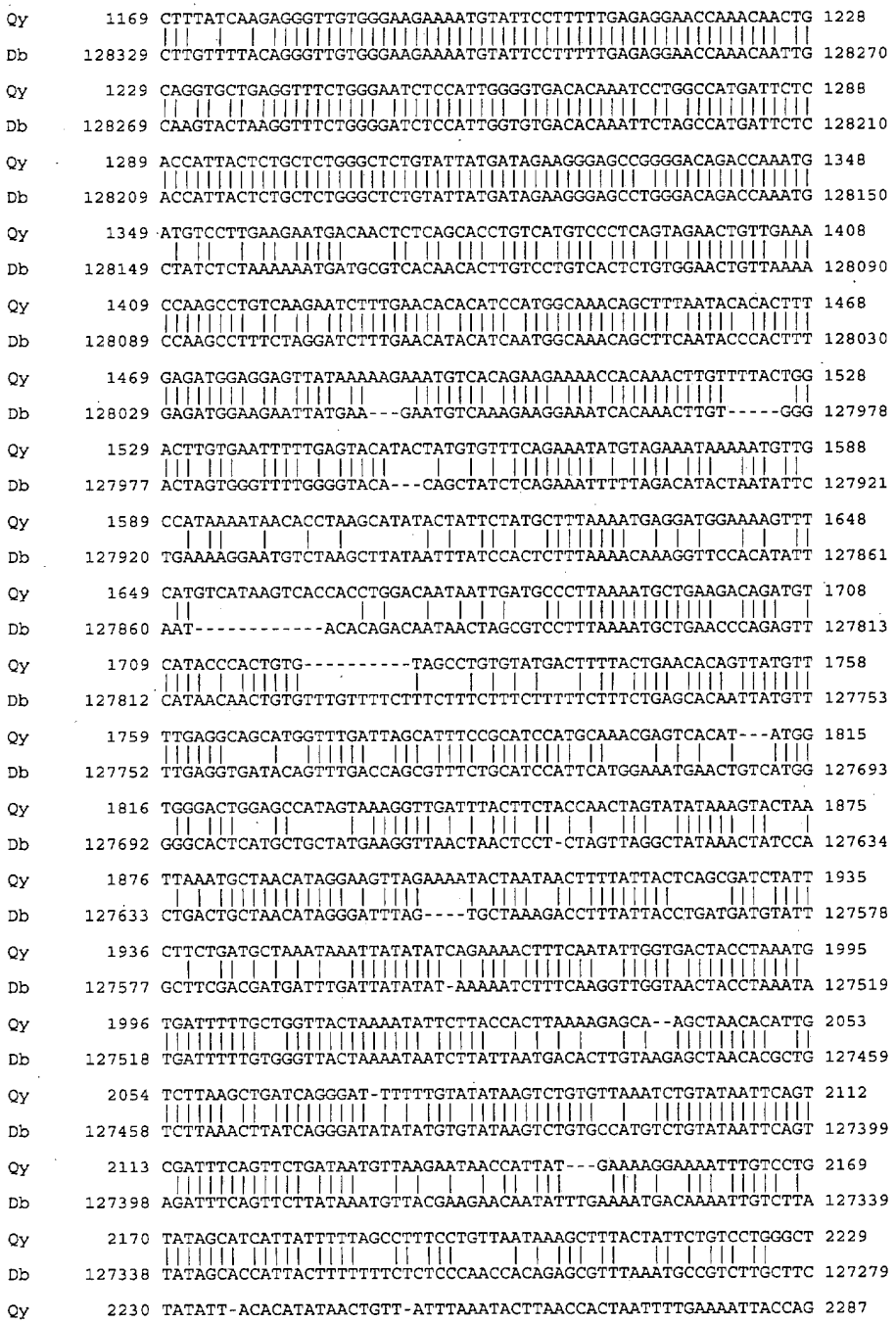
ORIGIN

Query Match 20.7%; Score 572.2; DB 2; Length 188638;
Best Local Similarity 68.9%; Pred. No. 4.9e-110;
Matches 1107; Conservative 0; Mismatches 413; Indels 87; Gaps 20;



RESULT 15
AC116288/c
LOCUS AC116288 221680 bp DNA linear HTG 20-NOV-2002
DEFINITION Rattus norvegicus clone CH230-400K6, *** SEQUENCING IN PROGRESS ***.
ACCESSION AC116288
VERSION AC116288.4 GI:25138201
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 221680)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,

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            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 221680)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 221680)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 20, 2002 this sequence version replaced gi:23617766.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GUEX
                Center clone name: CH230-400K6
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 208260 bases at least Q40
                Consensus quality: 210450 bases at least Q30
                Consensus quality: 211791 bases at least Q20
                Estimated insert size: 216772; sum-of-contigs estimation
                Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1   221680: contig of 221680 bp in length.
FEATURES            Location/Qualifiers
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                    clone_end:T7"
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                    site:
                    end_sequence:BZ226538"
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                    clone_end:Sp6"
ORIGIN

  Query Match             20.7%;  Score 572.2;  DB 2;  Length 221680;
  Best Local Similarity   68.9%;  Pred. No. 4.9e-110;
  Matches 1107;  Conservative    0;  Mismatches  413;  Indels   87;  Gaps   20;

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Db      13089 CTTGTTTTACAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAATTG 13030

Qy       1229 CAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTC 1288
Db      13029 CAAGTACTAAGGTTTCTGGGGATCTCCATTGGTGTGACACAAATTCTAGCCATGATTCTC 12970

Qy       1289 ACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCGGGGACAGACCAAATG 1348
Db      12969 ACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATG 12910

Qy       1349 ATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAA 1408
Db      12909 CTATCTCTAAAAAATGATGCGTCACAACACTTGTCCTGTCACTCTGTGGAACTGTTAAAA 12850

Qy       1409 CCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTT 1468
Db      12849 CCAAGCCTTTCTAGGATCTTTGAACATACATCAATGGCAAACAGCTTCAATACCCACTTT 12790

Qy       1469 GAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTACTGG 1528
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Db      12680 TGAAAAGGAATGTCTAAGCTTATAATTTATCCACTCTTTAAAACAAAGGTTCCACATATT 12621

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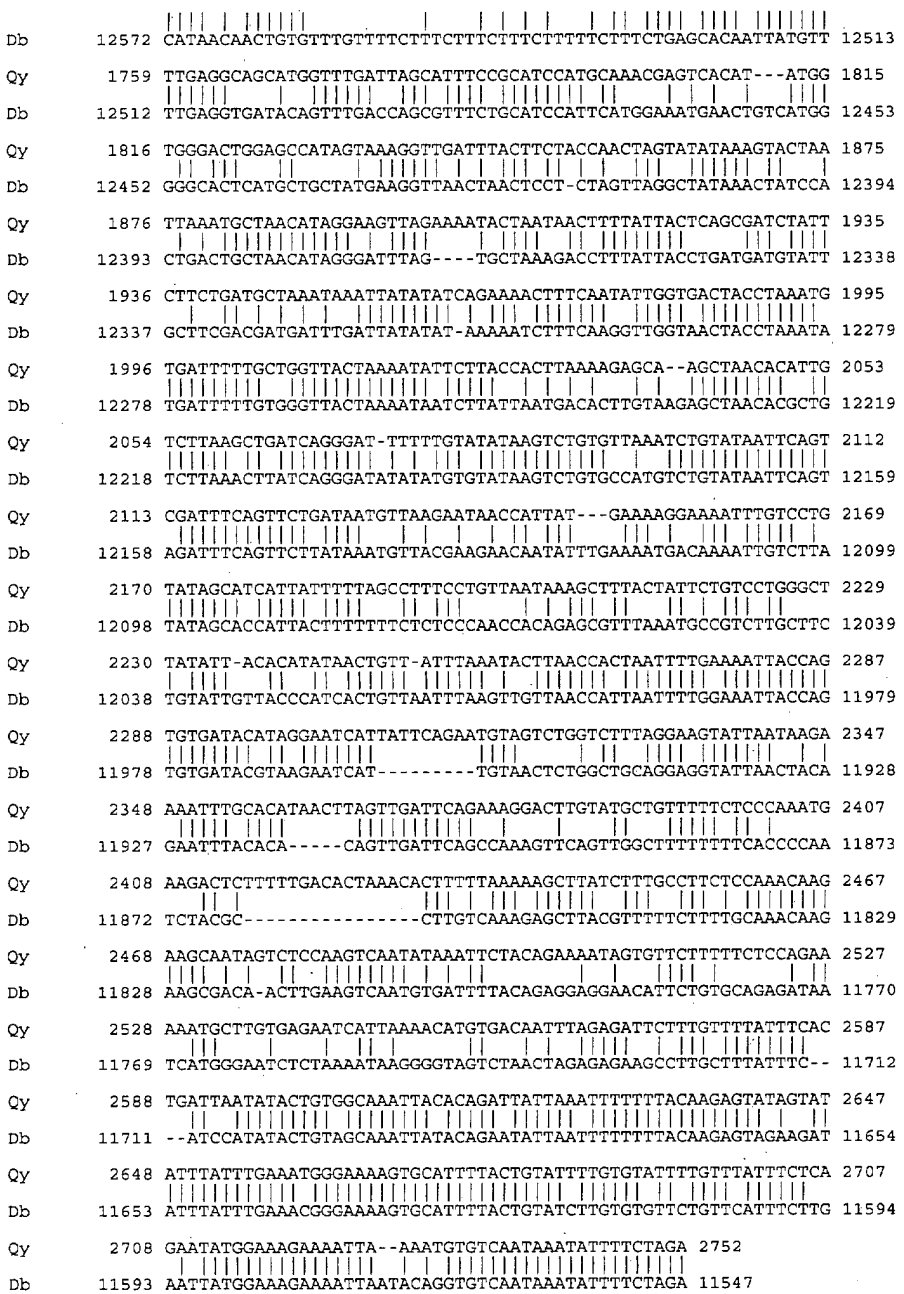

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